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200714

M 2

STIC-Biotech/ChemLib

From: Seharaseyon, Jegatheesan
Sent: Wednesday, September 06, 2006 10:29 AM
To: STIC-Biotech/ChemLib
Subject: Re: 10/659684

Hi,
Please search SEQ ID NO: 2 and 115 of 10/659684 in the commercial database.
Thanks.

Seyon.

J. Seharaseyon
Remsen 4C61,
Box 4C70.

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 9-7-06
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:39:36 ; Search time 67.1143 Seconds
(without alignments)
1103.626 Million cell updates/sec

Title: US-10-659-684-2

Perfect score: 850
Sequence: 1 MRSSPGMEXIVICLMVIFL.....LLOKMIHQHLSRTHSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_8:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*
9: geneeqp2005s:*
10: geneeqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	850	100.0	162	3 AAB18623	Aab18623 A human z
2	850	100.0	162	5 AAE13729	Aae13729 Human sol
3	850	100.0	162	5 AAU11965	Aau11965 Human int
4	850	100.0	162	6 ABR61407	Abrr61407 Human IL-
5	850	100.0	162	7 AAE14932	Aae14932 Human int
6	850	100.0	162	7 ABU62893	Abu62893 Human int
7	850	100.0	162	7 ADE85808	Ade85808 Human int
8	850	100.0	162	7 ADF17046	Adf17046 Human alb
9	850	100.0	162	7 ADH44572	Adh44572 Human zai
10	850	100.0	162	7 ADI00908	Adi00908 Immunity-
11	850	100.0	162	8 ADH10501	Adh10501 Human int
12	850	100.0	162	8 ADJ25621	Adj25621 Human int
13	850	100.0	162	8 ADM41017	Adm41017 Human IL-
14	850	100.0	162	8 ADP12563	Adp12563 Protein e
15	850	100.0	162	8 ADP19731	Adp19731 Human zai
16	850	100.0	162	8 ADP70459	Adp70459 Human int
17	850	100.0	162	8 ADS19031	Ads19031 Full leng
18	850	100.0	162	9 ADV96355	Adv96355 Human zai
19	850	100.0	162	9 ADY20419	Ady20419 PRO polyp
20	850	100.0	162	9 ADY17792	Ady17792 PRO polyp
21	850	100.0	162	9 ADZ20501	Adz20501 Human int
22	850	100.0	162	9 AEB26428	Aeb26428 Human int
23	850	100.0	162	9 AED68671	Aed68671 Human int

24	850	100.0	162	10 AEB19679	Aeb19679 Human int
25	850	100.0	162	10 AEG05273	Aeg05273 Human IL-
26	840	98.8	160	9 AEA52828	Aea52828 Human int
27	837	98.5	162	8 ADY27249	Ady27249 Human int
28	831	97.8	162	7 AAE14934	Aae14934 Human int
29	758	89.2	147	7 AAE14933	Aae14933 Human int
30	708.5	83.4	742	7 ADF17042	Adf17042 Human alb
31	706	83.1	133	9 ADM43687	Adm43687 Mature hu
32	706	83.1	134	8 ADP70485	Adp70485 Codon opt
33	695.5	81.8	519	8 AAB18627	Aab18627 Ami.no aci
34	695.5	81.8	519	5 AAU11971	Aau11971 MBP-human
35	695.5	81.8	519	7 ADH44655	Adh44655 Human zai
36	695.5	81.8	519	7 ADI00991	Adi00991 MBP (mat
37	695.5	81.8	519	8 ADP19814	Adp19814 Human zai
38	695.5	81.8	519	8 ADV96438	Adv96438 Human zai
39	695	81.8	131	8 ADS19023	Ads19023 Mature hu
40	695	81.8	131	9 ADM43684	Adm43684 Predicted
41	695	81.8	131	10 AEB19672	Aeb19672 Mature hu
42	661	77.8	133	9 ADM43680	Adm43680 Human int
43	656	77.2	133	9 ADM43682	Adm43682 Human int
44	650	76.5	131	9 ADM43678	Adm43678 Human int
45	648	76.2	152	10 AEB19682	Aeb19682 Bovine In

ALIGNMENTS

RESULT 1	AA18623	standard; protein; 162 AA.
ID	AA18623	
XX	AA18623	
AC	AA18623	
XX	AA18623	
DT	22-JAN-2001	(first entry)
XX	22-JAN-2001	
DE	A human zalphal1 ligand polypeptide.	
XX	zalphal1 ligand; cytokine; haematopoietic cell proliferation; lymphoma;	
KW	tumorigenesis; leukaemia; hematopoiesis; B cell tumour.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200053761-A2.	
PD	14-SEP-2000.	
XX		
PF	09-MAR-2000; 2000WC-US006067.	
XX		
PR	09-MAR-1999; 99US-00264908.	
PR	11-MAR-1999; 99US-00265992.	
PR	01-JUL-1999; 99US-0142013P.	
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Novak JE, Presnell SR, Sprecher CA, Foeter DC, Holly RD;	
XX	Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;	
DR	WPI: 2000-565600/52.	
XX	N-PSDB; AAA75552.	
PT	New human cytokine, designated zalphal1 ligand, useful for stimulating	
PT	the proliferation and/or development of hematopoietic cells in vitro and	
PT	in vivo, and for treating tumorigenesis.	
XX		
PS	Disclosure; Page 205-206; 256pp; English.	
XX		
CC	The present sequence represents a human zalphal1 ligand polypeptide,	
CC	which is a cytokine. The zalphal1 ligand is useful for stimulating the	
CC	proliferation and development of haematopoietic cells in vitro and in	
CC	vivo. Zalphal1 ligand polynucleotides can be used as primers or probes	
CC	for cloning the zalphal1 gene. The zalphal1 ligand is useful for treating	
CC	tumorigenesis. A zalphal1 ligand-aporin fusion toxin may be used for	
CC	treating leukaemia and lymphomas. Antagonists against zalphal1 ligand	

CC are useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalphall ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphall ligand
CC genetic defect
XX
SQ Sequence 162 AA;

Query Match 100.0%; Score 850; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLAWIFLGLTVHKSSSGQGDHMRMRQLIDIVDLKKNYNDLVPF 60
DB 1 MRSSPGNMERIVICLAWIFLGLTVHKSSSGQGDHMRMRQLIDIVDLKKNYNDLVPF 60
QY 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSITKUKRKPSTNAGRORHRL 120
DB 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSITKUKRKPSTNAGRORHRL 120
QY 121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 2

AAE13729
ID AAE13729 standard; protein; 162 AA.

XX AAE13729;
AC 26-FEB-2002 (first entry)

DE Human soluble zalphall cytokine receptor ligand protein.

XX Human; zalphall; cytokine receptor; immunosuppressive; cytostatic;
XX inflammatory disorder; haemostatic; cell proliferation; immune disorder;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
XX ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
XX viral infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..31 /label= Signal_peptide

FT Protein 32..162 /label= Mature_zalphall_ligand

FT Region 41..56 /label= Helix_A

FT Region 69..84 /label= Helix_B

FT Region 92..105 /label= Helix_C

FT Region 135..148 /label= Helix_D

FT Region 136..138 /note= "Conserved region"

XX WO200177171-A2.

XX 18-OCT-2001.

XX 03-APR-2001; 2001WO-US010872.

XX 05-APR-2000; 2000US-0194731P.

XX 28-JUL-2000; 2000US-0222121P.

PA (ZYMO) ZYMOGENETICS INC.

PI Sprechter CA, Novak JE, West JW, Preenell SR, Holly RD, Nelson AJ;

XX WPI; 2002-025898/03.

DR N-PSDB; AAD22923.

XX Novel soluble receptor polypeptides and polynucleotides used as cytokine

PT antagonist for stimulating ligand activity-induced proliferation of

XX hematopoietic cells and for suppressing immune response in a mammal.

XX Claim 1; Page 181; 243pp; English.

CC The invention relates to an isolated soluble zalphall cytokine receptor
CC polypeptide and their cDNA molecules. Zalphall proteins are useful for
CC inhibiting or antagonising the ligand activity-induced proliferation of
CC hematopoietic cells and haematopoietic cell progenitors preferably
CC lymphoid cells which are natural killer cells or cytotoxic T cells.
CC Zalphall is useful for treating immune and inflammatory disorders, for
CC reducing proliferation of neoplastic B or T cells, for suppressing an
CC immune response in a mammal exposed to an antigen or pathogen. Zalphall
CC is useful for treating diseases that require immune regulation including
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC sepsis, viral infection (dengue virus infection) and cancer. The present
CC sequence is human soluble zalphall cytokine receptor ligand

XX SQ Sequence 162 AA;

Query Match 100.0%; Score 850; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLAWIFLGLTVHKSSSGQGDHMRMRQLIDIVDLKKNYNDLVPF 60
DB 1 MRSSPGNMERIVICLAWIFLGLTVHKSSSGQGDHMRMRQLIDIVDLKKNYNDLVPF 60
QY 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSITKUKRKPSTNAGRORHRL 120
DB 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSITKUKRKPSTNAGRORHRL 120
QY 121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 3

AAU11965
ID AAU11965 standard; protein; 162 AA.

XX AAU11965;

XX 09-APR-2002 (first entry)

DE Human zalphall ligand polypeptide.

XX Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;
XX natural killer cell proliferation; T-cell proliferation;
XX B-cell proliferation; anti-tumour response; immune system;
XX immunostimulant; cytostatic; human; hPBGS;
XX activated human peripheral blood cell.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..31 /label= Signal_peptide

FT Protein 32..162 /label= Mature_zalphall_ligand

XX US6307024-B1.

PD	23-OCT-2001.
XX	
PF	
09-MAR-2000;	2000US-00522217.
XX	
09-MAR-1999;	99US-0123547P.
PR	11-MAR-1999;
PR	01-JUL-1999;
PR	99US-0142013P.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
XX	
XX	
PI	Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
P1	Gross JA, Johnson JV, Nelson AJ, Dillon SR, Hammond AK;
XX	
DR	WPI; 2002-040208/05.
DR	N-PSDB; AAS20637.
XX	
PT	New zalphall ligand polypeptides and polynucleotides, useful for
PT	stimulating proliferation, activation, differentiation and/or induction
PT	of inhibition of specialized cell function, or for stimulating an
PT	antigenic response.
XX	
PS	Claim 7; Col 125-126; 105pb; English.
XX	
CC	The present invention relates to the isolation of a novel cytokine,
CC	zalphall ligand and the polynucleotide encoding it. The invention also
CC	gives the sequence for the zalphall receptor and the polynucleotide
CC	encoding it. The zalphall ligand polypeptide stimulates proliferation of
CC	natural killer (NK) cells or NK cell progenitors, the activation of NK
CC	cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC	anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC	reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
CC	zalphall ligand polypeptide is also useful in preparing antibodies that
CC	bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can
CC	be used as probes or primers to clone regions of a zalphall ligand gene,
CC	and in gene therapy. Zalphall ligand may also be used to identify
CC	inhibitors of its activity, to enhance the generation of anti-tumour
CC	responses with or without the infusion of donor lymphocytes, and to
CC	activate or stimulate the immune system. The present sequence represents
CC	human zalphall ligand polypeptide. The cDNA encoding this is isolated
CC	from a cDNA library from activated human peripheral blood cells (hpBCs)
CC	
SQ	Sequence 162 AA;
	Query Match 100.0%; Score 850; DB 5; Length 162;
	Best Local Similarity 100.0%; Pred. No. 2e-86;
	Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 MRSSGNNRRIYICLMTVIFLGTILVHKSSQGGDRMIMRQLIDIVDQKATYNDLVBEF 60
DB	1 MRSSGNNRRIYICLMTVIFLGTILVHKSSQGGDRMIMRQLIDIVDQKATYNDLVBEF 60
OY	61 LPAPDVTNCEWMSAFSCFOKAKQLSANTGNNRIINYSIKKLKRPSTNAGRQKRL 120
DB	61 LPAPDVTNCEWMSAFSCFOKAKQLSANTGNNRIINYSIKKLKRPSTNAGRQKRL 120
OY	121 TCPSCDSYEKKPKKEFLERFKSLQKMIHQHLSSTRHSGEDS 162
DB	121 TCPSCDSYEKKPKKEFLERFKSLQKMIHQHLSSTRHSGEDS 162
RESULT 4	
ID	ABR61407
XX	ABR61407 standard; protein; 162 AA.
AC	ABR61407;
XX	
DT	12-AUG-2003 (first entry)
XX	
DE	Human IL-21 SEQ ID NO:19.
XX	
KM	arthritis; disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
KM	immune cell activity; cancer; infectious disorder; antineumatic;
KM	antiarthritic; osteopathic; antipsoaritic; cytostatic; antibacterial;

KM vinclole; antiparasitic; immunosuppressive; antidiabetic; dermatological
 KW neuroprotective; anticancer; antiallergic; antianemic; hepatotropic;
 KW antithyroid; antinflammatory; immune response; immune disorder;
 KW autoimmune disease; human.
 XX
 XX Homo sapiens.
 OS
 XX WO2003028630-A2.
 PN
 XX 10-APR-2003.
 PD
 XX
 XX 04-OCT-2002; 2002WO-US029839.
 PF
 XX
 XX 04-OCT-2001; 2001US-00972218.
 PR 17-APR-2002; 2002US-0373746P.
 XX
 XX
 XX (AMHP) WYETH.
 PA
 PI Carter L, Whiters MJ, Collins M, Young DA, Larsen G;
 PI Donaldson DD, Lowe LD, Dunussi K, Ma M, Witek JS, Kasalan MT;
 PI Ungar M;
 XX
 DR WPI; 2003-430146/40.
 DR N-PSDB; ACC80873.
 XX
 XX Treating or preventing arthritic disorder, cancer or infectious disorders
 PT in a subject, involves administering a modulator of interleukin-21 or its
 PT receptor which modulate immune cell activity.
 XX
 XX
 PS Disclosure; Page 37; 176pp; English.
 XX
 XX The invention relates to a novel method for treating or preventing an
 CC arthritic disorder in a subject. The method involves administering to the
 CC subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist
 CC optionally in combination with another therapeutic agent, to inhibit or
 CC reduce immune cell activity in the subject. The method is also useful for
 CC treating or preventing cancer or an infectious disorder, in a subject, by
 CC administering IL-21/IL-21R agonist, to increase immune cell activity. The
 CC method of the invention has antirheumatic, antiarthritic, osteopathic,
 CC antiparasitic, cytostatic, antibacterial, virucide, antiparasitic,
 CC immunosuppressive, antidiabetic, neuroprotective, dermatological,
 CC anticancer, antiallergic, antianemic, hepatotropic,
 CC antithyroid, and antinflammatory activity. The method is useful for
 CC treating or preventing an arthritic disorder such as Rheumatoid
 CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
 CC arthritis or ankylosing spondylitis, and also cancer such as solid
 CC tumour, soft tissue tumour or metastatic lesion, or an infectious
 CC disorder such a bacterial, viral or parasitic infection in a mammal,
 CC preferably human. A method of the invention is also is useful for
 CC increasing the ability of a vaccine composition containing an antigen to
 CC elicit a protective immune response in a subject against the antigen.
 CC The antigen is from a pathogen such as virus, bacterium or protozoan, or
 CC from cancer or tumour cell antigen, or expressed on the surface of cancer
 CC cell. An alternative method of the invention is useful for modulating the
 CC activity of immune or haematopoietic cells and thus to treat or prevent a
 CC variety of immune disorders, such as autoimmune diseases, for example
 CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus
 CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,
 CC hepatitis, Graves's disease, graft versus host disease, and scleroderma.
 CC The present process is used in an exemplification of the invention
 XX
 XX
 SO Sequence 162 AA:
 Query Match 100.0%; Score 850; DB 6; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSGNNRIVICLMVIFLGLTVHKSSGQGDHRMIRMROLIDVQLKYNVDLVEF 60
 Db 1 MRSSGNNRIVICLMVIFLGLTVHKSSGQGDHRMIRMROLIDVQLKYNVDLVEF 60
 QY 61 LPAPDVTNENWAFSCFGQAOLKSANTGNNRINIVSIKKLRKPPSTNAGRQRRL 120
 |||

Db 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNNERIIVSIIKKLKRKPPSTNAGRQKHRL 120
 QY 121 TCPSCDSYEKKPPKEFLERFKSLLOKMIHQHLSRTHGSEDS 162
 Db 121 TCPSCDSYEKKPPKEFLERFKSLLOKMIHQHLSRTHGSEDS 162
 RESULT 5
 AAE14932
 ID AAE14932 standard; protein, 162 AA.
 AC AAE14932;
 DT 27-AUG-2003 (first entry)
 DE Human interleukin-21 (IL-21).
 XX Interleukin-21; IL-21; antagonist; cancer; inflammatory;
 KM autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; myasthenia gravis; diabetes; human;
 KM zalphall ligand.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Region 41..56
 FT /label= Helix_A
 FT Binding-site 44
 FT /note= "Important for IL-21 binding to its receptor"
 FT Binding-site 47
 FT /note= "Important for IL-21 binding to its receptor"
 FT Region 57..68
 FT /label= A/B_loop
 FT Region 69..84
 FT /label= Helix_B
 FT Region 85..91
 FT /label= B/C_loop
 FT Region 92..105
 FT /label= Helix_C
 FT Region 106..134
 FT /label= C/D_loop
 FT Region 135..148
 FT /label= Helix_D
 FT Binding-site 135
 FT /note= "Important for IL-21 binding to its receptor"
 FT
 XX WO2003040313-A2.
 PN 15-MAY-2003.
 XX
 PD 28-OCT-2002; 2002WO-US034502.
 XX
 PF 05-NOV-2001; 2001US-0337586P.
 XX
 PR (ZYMO) ZYMOGENETICS INC.
 XX
 PA Presnell SR, West JW, Novak JE;
 XX WPI; 2003-441547/41.
 DR N-PSDB; AAD47852.
 XX
 XX New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
 PT and treating disorders with aberrant expression or activity of the IL-21
 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
 PT diabetes.
 XX
 PS Disclosure; Page 53-54; 71pp; English.
 XX
 CC The invention relates to polynucleotides and polypeptides of interleukin-
 CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
 CC that is not detectable in receptor binding studies. The antagonists of
 CC the invention have mutations in the D helix of the IL-21 molecule, and
 CC can be used to inhibit the activity of IL-21 with its cognate receptor.

CC The IL-21 antagonists are useful for diagnosing and treating disorders
 CC involving the aberrant expression or activity of the IL-21 polypeptide,
 CC such as cancer, inflammatory and autoimmune disorders, including
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
 CC myasthenia gravis and diabetes. The polypeptides can also be used to
 CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
 CC and for enhancing in vivo killing of target tissues. The present sequence
 CC is human IL-21 (originally designated zalphall ligand)
 CC
 XX
 SQ Sequence 162 AA:
 Query Match 100.0%; Score 850; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGNMERIVICLWVIFIGTLVHKSSSGODRHMIRMQLDIDYDQKNYNDLVPEF 60
 Db 1 MRSSPGNMERIVICLWVIFIGTLVHKSSSGODRHMIRMQLDIDYDQKNYNDLVPEF 60
 QY 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNNERIIVSIIKKLKRKPPSTNAGRQKHRL 120
 Db 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNNERIIVSIIKKLKRKPPSTNAGRQKHRL 120
 QY 121 TCPSCDSYEKKPPKEFLERFKSLLOKMIHQHLSRTHGSEDS 162
 Db 121 TCPSCDSYEKKPPKEFLERFKSLLOKMIHQHLSRTHGSEDS 162
 RESULT 6
 ABU62893
 ID ABU62893 standard; protein, 162 AA.
 XX
 AC ABU62893;
 DT 15-SEP-2003 (first entry)
 DE Human interleukin 21 (IL-21).
 XX
 KM Human, MU-1; haematopoietin receptor superfamily chain; immunomodulator;
 KM cytosolic; antibacterial; virucide; antianaemic; gene therapy;
 KM hematopoiesis; anaemias; immune response; cancer; infection;
 KM transplanted organ; cytokine; receptor; interleukin 21; IL21.
 XX
 OS Homo sapiens.
 XX
 XX US2003049798-A1.
 PN 13-MAR-2003.
 PD 04-OCT-2001; 2001US-00972218.
 XX
 PF 17-MAR-1998; 98US-00040005.
 PR 28-APR-2000; 2000US-00560766.
 PR 11-MAY-2000; 2000US-00569384.
 XX
 PA (CART/) CARTER L.
 PA (WHIT/) WHITTERS M J.
 PA (COLL/) COLLINS M.
 PA (YOUN/) YOUNG D A.
 PA (DONA/) DONALDSON D D.
 PA (LOWE/) LOWE L D.
 PA (UNGE/) UNGER M.
 XX
 PI Carter L, Whitters M, Collins M, Young DA, Donaldson DD;
 PI Lowe LD, Unger M;
 XX
 DR WPI; 2003-512354/48.
 DR N-PSDB; ACD26729.
 XX
 XX New fusion polypeptide for regulating hematopoiesis and immune responses,
 PT comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion
 PT polypeptide.

PS Disclosure; Page 10; 26pp; English.

XX The invention describes a fusion polypeptide comprising at least a
CC fragment of a WO-1 polypeptide and a non-WO-1 fusion polypeptide. The
CC polypeptide is useful in regulating haematopoiesis (e.g. in cases of
CC anaemias) and/or immune responses (e.g. immune response to cancer,
CC infections or to a transplanted organ) and in identifying other members
CC of the haematopoietic superfamily, including cytokines and receptors. The
CC polynucleotide may be used to express recombinant protein for analysis,
CC characterisation or therapeutic use; and as markers for tissues or
CC chromosomes. The polypeptide and polynucleotide may also be used as
CC nutritional sources or supplements. This is the amino acid sequence of
CC human interleukin 21 (IL21), a cytokine receptor that can be used to
CC characterise the novel haematopoietic receptor of the invention

XX Sequence 162 AA;

Query Match 100.0%; Score 850; DB 7; Length 162;

Best Local Similarity 100.0%; Pred. No. 2e-86; Mismatches 0; Indels 0; Gaps 0;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQDRHMRMQLIDIVDLKNYVNDLVPEF 60

Db 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQDRHMRMQLIDIVDLKNYVNDLVPEF 60

QY 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRORGRRL 120

Db 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRORGRRL 120

QY 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162

Db 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162

RESULT 7

ID ADE85808 standard; protein; 162 AA.

AC ADE85808;

DT 29-JAN-2004 (first entry)

DE Human interleukin-21.

XX Human; interleukin-21; immunosuppressive; antitumour; antiarthritic;

KW antiinflammatory; dermatological; ophthalmological; uteropathic;

KW muscular-gen.; vasotropic; antidiabetic; antihypertensive; thymic;

XX neuroprotective; gastrointestinal-gen.; antipneumatic; gene therapy.

OS Homo sapiens.

PN WO2003087320-A2.

XX 23-OCT-2003.

PF 08-APR-2003; 2003WO-US010736.

PR 09-APR-2002; 2002US-0371038P.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

PI Mo11 T, Strom TB, Zheng XX;

DR WPI; 2003-845317/78.

XX New substantially pure interleukin-21 polypeptide, useful for diagnosing,

PT treating and prognosticating autoimmune disorders, e.g. rheumatic

PT disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis

PT and myasthenia gravis.

PS Disclosure; SEQ ID NO 1; 65pp; English.

XX The present sequence is the protein sequence of human interleukin-21 (IL-

CC 21). The invention provides antagonists of the IL-21 receptor. These

CC include mutants of murine IL-21 in which the Gln residue at position 119

CC of the mature polypeptide is substituted by Asp or in which the Gln

CC residues at positions 114 and 119 of the mature polypeptide are both

CC replaced by Asp. The mutant IL-21 polypeptides inhibit or suppress T-cell

CC activation. They preferably comprise a sequence that increases

CC circulating half-life, such as the FC region of an IgG molecule and may

CC further comprise an antigenic tag. Such antagonists inhibit cellular

CC proliferation in response to either anti-CD3 monoclonal antibodies or

CC anti-CD3 antibodies applied together with IL-2 and/or IL-15 together with

CC IL-21. A claimed method of suppressing the immune response in a patient

CC comprises administering the IL-21 antagonist or a nucleic acid encoding

CC it. The method is used to treat an autoimmune disease such as rheumatic

CC disease, including systemic lupus erythematosus, Sjogren's syndrome,

CC scleroderma, mixed connective tissue disease, dermatomyositis,

CC polymyositis, Reiter's syndrome, or Bence's disease, or rheumatoid

CC arthritis, type I diabetes, autoimmune disease of the thyroid such as

CC Hashimoto's thyroiditis or Graves' disease, an autoimmune disease of the

CC central nervous system such as multiple sclerosis, myasthenia gravis, or

CC encephalomyelitis, or an autoimmune disease selected from pemphigus

CC vulgaris, pemphigus vegetans, pemphigus foliaceus, Senear-Usher syndrome,

CC Brazilian pemphigus, psoriasis or inflammatory bowel disease (all

CC claimed).

CC Sequence 162 AA;

Query Match 100.0%; Score 850; DB 7; Length 162;

Best Local Similarity 100.0%; Pred. No. 2e-86; Mismatches 0; Indels 0; Gaps 0;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQDRHMRMQLIDIVDLKNYVNDLVPEF 60

Db 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQDRHMRMQLIDIVDLKNYVNDLVPEF 60

QY 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRORGRRL 120

Db 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRORGRRL 120

QY 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162

Db 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162

RESULT 8

ID ADF17046

ADFL7046 standard; protein; 162 AA.

AC ADF17046;

DT 12-FEB-2004 (first entry)

DE Human albumin fusion protein-related protein SegID2177.

XX albumin fusion protein; albumin activity; human serum albumin;

KW serum osmotic pressure; shelf-life; stability; antidiabetic;

KW gene therapy; diabetes mellitus; human; gene; ds.

OS Homo sapiens.

PN WO2003060071-A2.

XX 24-JUL-2003.

PF 23-DEC-2002; 2002WO-US040891.

PR 21-DEC-2001; 2001US-0341811P.

PR 24-JAN-2002; 2002US-0350358P.

PR 28-JAN-2002; 2002US-0351360P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370237P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.
 PR 26-MAY-2002; 2002US-0383123P.
 PR 05-JUN-2002; 2002US-0385708P.
 PR 10-JUL-2002; 2002US-0394625P.
 PR 24-JUL-2002; 2002US-0398008P.
 PR 09-AUG-2002; 2002US-0402131P.
 PR 13-AUG-2002; 2002US-0402708P.
 PR 18-SEP-2002; 2002US-0411355P.
 PR 18-SEP-2002; 2002US-0411426P.
 PR 02-OCT-2002; 2002US-0414984P.
 PR 11-OCT-2002; 2002US-0417611P.
 PR 23-OCT-2002; 2002US-0420246P.
 PR 05-NOV-2002; 2002US-0423623P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (DELTA) DELTA BIOTECHNOLOGY LTD.
 PA (PRIN-) PRINCIPIA PHARM CORP.
 XX
 PI Balance DJ, Turner AJ, Rosen CA, Haseltine WA;
 XX
 XX WPI, 2003-598517/56.
 DR N-PSDB; ADF17040.
 XX
 XX New albumin fusion protein, useful for preparing a composition for
 PT treating diabetes mellitus.
 XX
 XX Example 4; SEQ ID NO 2177; 24pp; English.
 XX
 XX This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is that of a therapeutic protein
 CC which was fused with human albumin to create a novel albumin fusion
 CC protein of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 162 AA;
 Query Match 100.0%; Score 850; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KM tumour progression; metastasis; tumour stasis; haematopoietic tumour;
 KM lymphoma; B cell tumour; systemic lupus erythematosus;
 KM rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;
 KM immunocompromised patient; HIV infection; vaccine; chromosome 4q27.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..31
 FT /note= "Signal peptide"
 FT Protein 32..162
 FT /note= "Mature Zalphall, claimed in claim 1"
 XX
 XX US6605272-B2.
 XX
 PD 12-AUG-2003.
 XX
 PF 03-AUG-2001; 2001US-00923246.
 XX
 PR 09-MAR-1999; 99US-0123547P.
 PR 11-MAR-1999; 99US-0123904P.
 PR 01-JUL-1999; 99US-0142013P.
 PR 09-MAR-2000; 2000US-00522217.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX
 XX WPI, 2003-895283/82.
 XX
 XX Stimulating an immune response in a mammal exposed to an antigen or
 PT pathogen, useful for enhancing anti-tumor activity resulting in reduced
 PT tumor progression or metastasis, comprises administering zalphall ligand
 PT polypeptide.
 XX
 XX Claim 1; SEQ ID NO 2; 103pp; English.
 XX
 XX The invention relates to stimulating an immune response in a mammal
 CC exposed to an antigen or pathogen comprising administering a composition
 CC comprising mature zalphall ligand polypeptide comprising residues 32-162
 CC of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an
 CC immune response in a mammal exposed to an antigen or pathogen
 CC (comprising: (a) determining (in)directly the level of antigen or
 CC pathogen present in the mammal; (b) administering a composition
 CC comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c)
 CC determining (in)directly the level of antigen or pathogen in the mammal;
 CC and (d) comparing the antigen or pathogen level in (a) with (b), where a
 CC change in the level indicates stimulation of immune response), and
 CC stimulating an immune response in a mammal exposed to an antigen or
 CC pathogen (comprising: (a) determining a level of antigen- or pathogen-
 CC specific antibody; (b) administering a composition comprising zalphall
 CC ligand polypeptide in a pharmaceutical vehicle; (c) determining a post
 CC administration level in the antigen- or pathogen-specific antibody; and
 CC (d) comparing the level of the antibody in (a) with (b), where an
 CC increase in the antibody level indicates stimulation of immune response).
 CC The method is useful for stimulating an immune response in a mammal
 CC exposed to an antigen or pathogen, and for enhancing anti-tumor activity
 CC resulting in a reduction in tumour progression, decrease in metastasis,
 CC or a tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma
 CC or a B cell tumour. The zalphall ligand is useful for treating a wide
 CC range of diseases arising from defects in the immune system, e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or
 CC diabetes, for boosting immunity to infectious diseases, treating
 CC immunocompromised patients, such as HIV+ patients and in improving
 CC vaccines. The present sequence is a human zalphall ligand protein.
 XX
 SQ Sequence 162 AA;
 Query Match 100.0%; Score 850; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	I	MRSFGNNRRIYICLMTVIFLGTLVHKSSQGDGRMIMRQLIDIVDOLKMYNDLVPEF	60
Dd	1	MRSFGNNRRIYICLMTVIFLGTLVHKSSQGDGRMIMRQLIDIVDOLKMYNDLVPEF	60
Oy	61	LPAEDVTNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKKPPSTNAGRQKHRL	120
Dd	61	LPAEDVTNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKKPPSTNAGRQKHRL	120
Oy	121	TCPSCDSEYEKKPKKEFLERFKSLQKMTHOHLSSRTHSDEDS	162
Dd	121	TCPSCDSEYEKKPKKEFLERFKSLQKMTHOHLSSRTHSDEDS	162
<p style="text-align:center;">RESULT 10 ADI00908 ADI00908 standard; protein; 162 AA.</p>			
ID	AD100908	standard; protein; 162 AA.	
XX	AD100908;		
XX	22-APR-2004	(first entry)	
XX	Immunlty-related human zalphall ligand protein.		
XX	zalphall ligand; immunity; infectious disease; immunocompromised patient;		
KW	HIV; vaccine; human.		
XX	Homo sapiens.		
OS	US2003125524-A1.		
PN	03-JUL-2003.		
XX	15-NOV-2002; 2002US-00295723.		
PF	09-MAR-2000; 2000US-00522217.		
XX	(ZYMO) ZYMOGENETICS INC.		
PA	Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;		
PI	Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;		
PI	WPI; 2003-811003/76.		
DR	N-PsDB; ADI00907.		
XX	New zalphall ligand polypeptides, useful for boosting immunity to		
PT	infectious diseases, and treating immunocompromised patients, such as		
PT	human immunodeficiency virus (HIV) patients, or in improving vaccines.		
XX	Claim 7; SEQ ID NO 2; 113PD; English.		
PS	The invention relates to a novel isolated zalphall ligand polypeptide.		
CC	The polypeptide of the invention may be useful for boosting immunity to		
CC	infectious diseases and treating immunocompromised patients, such as HIV		
CC	patients, as well as in improving vaccines. The current sequence is that		
CC	of the human zalphall ligand protein of the invention.		
XX	Sequence 162 AA:		
SQ			
<p style="text-align:center;">Query Match 100.0%; Score 850; DB 7; Length 162; Best Local Similarity 100.0%; Pred. No. 2e-86; Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>			
Oy	1	MRSFGNNRRIYICLMTVIFLGTLVHKSSQGDGRMIMRQLIDIVDOLKMYNDLVPEF	60
Dd	1	MRSFGNNRRIYICLMTVIFLGTLVHKSSQGDGRMIMRQLIDIVDOLKMYNDLVPEF	60
Oy	61	LPAEDVTNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKKPPSTNAGRQKHRL	120
Dd	61	LPAEDVTNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKKPPSTNAGRQKHRL	120
Oy	121	TCPSCDSEYEKKPKKEFLERFKSLQKMTHOHLSSRTHSDEDS	162
Dd	121	TCPSCDSEYEKKPKKEFLERFKSLQKMTHOHLSSRTHSDEDS	162

	RESULT 11
ID	ADH10501
XX	ADH10501 standard; protein; 162 AA.
AC	ADH10501:
XX	
D7	11-MAR-2004 (first entry)
XX	
DE	Human interleukin-21 (IL-21) polypeptide.
XX	
KM	IL-21: interleukin-21; cytostatic; virucide; anti-inflammatory; hepatotropic; neuroprotective; muscular; respiratory; antithrombotic; antibacterial; anti-HIV; gene therapy; cancer; human.
XX	
OS	Homo sapiens.
FH	
FT	Key Location/Qualifiers
FT	Peptide /note= "specifically claimed fragment"
FT	Peptide 41..148 /note= "specifically claimed fragment"
XX	
PM	M02003I03589-AA.
PD	
XX	18-DEC-2003.
Pf	06-JUN-2003; 2003MO-US017808.
PR	07-JUN-2002; 2002US-0387127P.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
PI	Nelson AJ, Hughes SD, Holly RD, Kindsvogel WR;
DR	WPI: 2004-062206/06. N-PDSB: ADH10500.
PT	Treating Non-Hodgkin's lymphoma, cancer or infection comprises administering to the subject a polypeptide having a functional activity of interleukin-21.
PS	Claim 9; SEQ ID NO 2; 154pp; English.
CC	The invention relates to treating Non-Hodgkin's lymphoma, cancer or infection and involves administering to the subject a polypeptide having a functional activity of interleukin-21 (IL-21). The methods are useful for treating Non-Hodgkin's lymphoma; cancer such as renal cell carcinoma, epithelial carcinoma, breast cancer, prostate cancer, ovarian cancer and colon cancer; viral infection such as AIDS, Hepatitis B or C virus, gastroenteritis, haemorrhagic diseases, enteritis, carditis, encephalitis, paralysis, bronchiolitis, upper or lower respiratory disease, respiratory papillomatosis, arthritis, disseminated disease, meningitis, and mononucleosis; or bacterial infection, such as an infection by a bacteria selected from chlamydiae, listeriae, helicobacterium, mycobacterium, mycoplasma, salmonella, and shigella, or sudden acute respiratory syndrome caused by a coronavirus, Herpes Simplex viruses, Epstein-Barr virus, Cytomegalovirus, Pox viruses, Papilloma virus, Adenovirus, Poliovirus, Orthomyxoviruses, Paramyxoviruses, Influenza viruses, caliciviruses, rabies viruses, and rinderpest viruses. The present sequence represents a human IL-21 polypeptide.
SQ	Sequence 162 AA: Query Match 100.0%; Score 850; DB 8; Length 162; Best Local Similarity 100.0%; Pred. No. 2e-86; Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 MRSSPGNNRRIYICLVMTFLGTVLVHKSSSGGODRRHMIRMLIDIVIQLKNRYNDLVPF 60 DB 1 MRSSPGNNRRIYICLVMTFLGTVLVHKSSSGGODRRHMIRMLIDIVIQLKNRYNDLVPF 60

QY 61 LPAPEDVETNCWSAFSCFOKAOLKSANTGNERRIIVNSIKKLKRKPPSTNAGRORGRRL 120
 DB 61 LPAPEDVETNCWSAFSCFOKAOLKSANTGNERRIIVNSIKKLKRKPPSTNAGRORGRRL 120
 QY 121 TCPSCDSYEKKPPEFLERFKSLQKMIHQHLSRTHGSEDS 162
 DB 121 TCPSCDSYEKKPPEFLERFKSLQKMIHQHLSRTHGSEDS 162
 RESULT 12
 ADJ25621
 ID ADJ25621 standard; protein; 162 AA.
 XX
 AC ADJ25621;
 XX
 XX 20-MAY-2004 (first entry)
 XX
 XX Human interleukin 21 (IL-21) protein SEQ ID NO:2.
 XX
 XX Interferon gamma inhibition; IFNgamma inhibition; interleukin 21 agonist;
 KM IL-21 agonist; antiasthmatic; antiallergic; antiarthritic; antirheumatic;
 KM neutroprotective; antiinflammatory; dermatological; immunosuppressive;
 KM muscular; antipneumonia; T helper; Th1; Th2; asthma; allergy;
 KM rheumatoid arthritis; multiple sclerosis; lupus; diabetes;
 KM Crohn's disease; psoriasis; myasthenia gravis; human; IL-21.
 XX
 XX Homo sapiens.
 OS
 XX WO2004007682-A2.
 PN
 XX 22-JAN-2004.
 PD
 XX 15-JUL-2003; 2003WO-US021975.
 PF
 XX 15-JUL-2002; 2002US-0396160P.
 PR
 XX 12-AUG-2002; 2002US-0403001P.
 XX
 XX (AMHP) WYETH.
 PA (HARD) HARVARD COLLEGE.
 PA
 XX Grusby M, Wurster A, Young DA, Collins M, Walters MJ;
 PI
 XX WPI: 2004-1122921/12.
 DR N-PSDB; ADJ25620.
 XX
 XX Inhibiting interferon gamma (IFNgamma) levels and T helper cell
 PT development and function in a T cell or cell population using IL-21
 PT modulators, useful for the preventing and/or treating asthma, allergy,
 PT arthritis, lupus and diabetes.
 XX
 XX Claim 1; SEQ ID NO 2; 59pp; English.
 PS
 XX The present invention describes a method for inhibiting interferon gamma
 CC (IFNgamma) levels in a T cell population by contacting the T cell or cell
 CC population with an interleukin 21 (IL-21) agonist in an amount sufficient
 CC to inhibit IFNgamma in the T cell or cell population, wherein the agonist
 CC is an IL-21 polypeptide comprising an amino acid sequence at least 85%
 CC identical to the 162 amino acids (SEQ ID NO: 2; ADJ25621), and which is
 CC capable of binding to an IL-21R. An IL-21 agonist has antiasthmatic,
 CC antiallergic, antiarthritic, antirheumatic, neuroprotective,
 CC antiinflammatory, dermatological, immunosuppressive, muscular and
 CC antipneumonia activities. The methods and compositions of the present
 CC invention are useful for the diagnosis, prevention and/or treatment of
 CC diseases or conditions associated with aberrant expression or activity of
 CC IL-21, T helper 1 (Th1) and/or Th2, such as asthma, allergy, allergic
 CC arthritis, multiple sclerosis, lupus, diabetes, Crohn's disease,
 CC psoriasis and myasthenia gravis. The present sequence represents human IL
 CC -21, which is used in the exemplification of the present invention.
 CC
 XX Sequence 162 AA;
 SQ

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGMERIVICLAWIFIGTLVHKSSSGODRHMIRMOQLDIVOLKNVNDLVPEF 60
 DB 1 MRSSPGMERIVICLAWIFIGTLVHKSSSGODRHMIRMOQLDIVOLKNVNDLVPEF 60
 QY 61 LPAPEDVETNCWSAFSCFOKAOLKSANTGNERRIIVNSIKKLKRKPPSTNAGRORGRRL 120
 DB 61 LPAPEDVETNCWSAFSCFOKAOLKSANTGNERRIIVNSIKKLKRKPPSTNAGRORGRRL 120
 QY 121 TCPSCDSYEKKPPEFLERFKSLQKMIHQHLSRTHGSEDS 162
 DB 121 TCPSCDSYEKKPPEFLERFKSLQKMIHQHLSRTHGSEDS 162
 RESULT 13
 ADM41017
 ID ADM41017 standard; protein; 162 AA.
 XX
 XX ADM41017;
 XX
 XX 15-JUL-2004 (first entry)
 DT
 XX
 XX Human IL-21 amino acid sequence, seq id 2.
 DE
 XX
 XX Antiallergic; antiasthmatic; antiparasitic; antiinflammatory;
 KM antihelminthic; dermatological; immunomodulatory; interleukin; IL-21;
 KM eosinophil; allergic; parasitic; asthma; allergic rhinitis;
 KM helminthic infection.
 XX
 XX Homo sapiens.
 OS
 XX WO2004032953-A1.
 PN
 XX 22-APR-2004.
 PD
 XX 13-OCT-2003; 2003WO-DK000691.
 PF
 XX 11-OCT-2002; 2002DK-00001546.
 PR 16-OCT-2002; 2002DK-00001587.
 PR 17-OCT-2002; 2002US-0419225P.
 XX
 XX (NOVO) NOVO NORDISK AS.
 PA
 XX Romer J, Moller NPH, Skak K;
 PI
 XX WPI: 2004-340821/31.
 DR
 XX Use of Interleukin-21 for the treatment of diseases or conditions where
 PT eosinophils are involved in a protective response in a subject, e.g.
 PT allergic conditions and/or parasitic diseases.
 XX
 XX Claim 6; SEQ ID NO 2; 32pp; English.
 PS
 XX The invention relates to an interleukin (IL)-21 that is used for the
 CC treatment of diseases or conditions where eosinophils are involved in a
 CC protective response in a subject, e.g. allergic conditions and/or
 CC parasitic diseases. Methods of the invention are useful for the treatment
 CC of diseases or conditions where eosinophils are involved in a protective
 CC response in a subject, such as allergic conditions (e.g. asthma, allergic
 CC rhinitis or allergic diseases of the skin) and/or parasitic diseases,
 CC especially helminthic infection. The current sequence represents the DNA
 CC sequence encoding IL-21. Note: This sequence is not encoded by that of
 CC ADM41016, which we are told in the specification is the IL-21 encoding
 CC nucleotide.
 XX
 XX Sequence 162 AA;
 SQ

Query Match 100.0%; Score 850; DB 8; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-86;

Query Match 100.0%; Score 850; DB 8; Length 162;

Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 MRSSPGNMERIVICLWVIFLGTIVHKSSSGQODRHMRMRLIDIVDLKXNVNDLVEF 60
Db 1 MRSSPGNMERIVICLWVIFLGTIVHKSSSGQODRHMRMRLIDIVDLKXNVNDLVEF 60
Oy 61 LPAPEDVETNCENSAFSCFOKAOLKSANTGNNERIINVISIKLKRKPPSTNAGRQKRL 120
Db 61 LPAPEDVETNCENSAFSCFOKAOLKSANTGNNERIINVISIKLKRKPPSTNAGRQKRL 120
Oy 121 TCPSCDSYEKKPPEKFLERFKSLLOKMIHOHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPPEKFLERFKSLLOKMIHOHLSRTHGSEDS 162
```

RESULT 14
ADP12563
ID ADP12563 standard; protein; 162 AA.

AC ADP12563;
XX

DT 12-AUG-2004 (first entry)
XX

DE Protein encoded by mRNA of the invention #173.
XX

XX transplamt rejection; immune system; rheumatoid arthritis; lupus;
KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

XX Homo sapiens.
XX

PN WO2004042346-A2.
XX

PD 21-MAY-2004.
XX

PF 24-APR-2003; 2003WO-US012946.
XX

PR 24-APR-2002; 2002US-00131831.
XX

PR 20-DEC-2002; 2002US-00325899.
XX

PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX

PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX

DR WPI; 2004-400724/37.
XX

PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX

PS Claim 65; SEQ ID NO 2572; 1762pp; English.
XX

CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX

XX Sequence 162 AA;
XX

Query Match 100.0%; Score 850; DB 8; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-86;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 MRSSPGNMERIVICLWVIFLGTIVHKSSSGQODRHMRMRLIDIVDLKXNVNDLVEF 60
Db 1 MRSSPGNMERIVICLWVIFLGTIVHKSSSGQODRHMRMRLIDIVDLKXNVNDLVEF 60
Oy 61 LPAPEDVETNCENSAFSCFOKAOLKSANTGNNERIINVISIKLKRKPPSTNAGRQKRL 120
Db 61 LPAPEDVETNCENSAFSCFOKAOLKSANTGNNERIINVISIKLKRKPPSTNAGRQKRL 120
Oy 121 TCPSCDSYEKKPPEKFLERFKSLLOKMIHOHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPPEKFLERFKSLLOKMIHOHLSRTHGSEDS 162
```

RESULT 15
ADP19731
ID ADP19731 standard; protein; 162 AA.

AC ADP19731;
XX

DT 26-AUG-2004 (first entry)
XX

DE Human zalphall ligand.
XX

XX cyrostatic; zalphall ligand; pharmaceutical; cancer; immune response;
KM melanoma; tumour; solid tumour; haematopoietic tumour; lymphoma; human;
KM chromosome 4.
XX

XX Homo sapiens.
XX

PN US2004110932-A1.
XX

PD 10-JUN-2004.
XX

PF 10-SEP-2003; 2003US-00659684.
XX

PR 09-MAR-1999; 99US-0123547P.
XX

PR 11-MAR-1999; 99US-0123904P.
XX

PR 01-JUL-1999; 99US-0142013P.
XX

PR 09-MAR-2000; 2000US-00522217.
XX

PA (ZYMO) ZYMOGENETICS INC.
XX

PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX

DR N-PSDB: ADP19730, ADP19732.
XX

DR WPI; 2004-440401/41.
XX

PT New zalphall ligand polynucleotide and polypeptide molecules, useful for
PT treating cancer, e.g. melanoma, solid tumor, hematopoietic tumor, or
PT lymphoma.
XX

PS Claim 1; SEQ ID NO 2; 111pp; English.
XX

CC The invention describes an isolated polypeptide comprising a sequence of
CC amino acid residues that is at least 90 or 95% identical to residues 41
CC (Gln) to 148 (Ile), or 32 (Gln) to 148 (Ile) of a sequence of 162 amino
CC acids (SEQ ID NO:2, human zalphall ligand), fully defined in the
CC specification. Also described are: a pharmaceutical composition
CC comprising the polypeptide, and a vehicle; a method of creating cancer in
CC a mammal; a method of stimulating an immune response in a mammal with
CC melanoma; a method of stimulating an immune response in a mammal bearing
CC a tumor; an isolated polynucleotide comprising a sequence of nucleotides
CC that encode amino acid residues cited above, where the polynucleotide
CC encodes a polypeptide that binds a receptor comprising 538 amino acids,
CC fully defined in the specification; a pharmaceutical composition
CC comprising the polynucleotide encoding, in a pharmaceutically acceptable
CC vehicle; an expression vector comprising the following operably linked
CC elements a control element; and a DNA segment comprising the
CC polynucleotide; and an isolated polynucleotide molecule comprising at
CC least 10 nucleotides of the polynucleotide sequence of 642 bp, fully
CC defined in the specification. The molecules, compositions and methods are

CC useful for treating cancer, e.g. melanoma, solid tumour, haematopoietic
 CC tumour, or lymphoma. This is the amino acid sequence of novel human
 CC cytokine zai1phail ligand.

XX
 SQ Sequence 162 AA;

Query Match 100.0%; Score 850; DB 8; Length 162;

Best Local Similarity 100.0%; Pred. No. 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRSSPGNMERIVICLWYIFLGTLVHKSSSGQDRHMIRMQLIDIVDQKNYVNDLVPEF	60
Db	1	MRSSPGNMERIVICLWYIFLGTLVHKSSSGQDRHMIRMQLIDIVDQKNYVNDLVPEF	60
QY	61	LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSITKLRKPPSTNAGRROKRL	120
Db	61	LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSITKLRKPPSTNAGRROKRL	120
QY	121	TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS	162
Db	121	TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS	162

Search completed: September 7, 2006, 12:44:57
 Job time : 69.1143 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:45:21 ; Search time 11.8029 Seconds
(without alignments)
1320.622 Million cell updates/sec

Title: US-10-659-684-2
Perfect score: 850
Sequence: 1 MRSSPGMERIVICLWVIFL.....LQKMHQHLSRRHSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.80.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94.5	11.1	162	1 A53484	interleukin-15 pre
2	91.5	10.8	567	2 S29498	lymphocyte antigen
3	83	9.8	899	2 B38529	nIB protein - Esc
4	82	9.6	607	1 ABXL72	74k albumin precu
5	79	9.3	206	2 S49882	hypothetical prote
6	78	9.2	741	2 UC7822	isocitrate dehydro
7	76.5	9.0	420	2 A25876	vitellinogen III p
8	76.5	9.0	864	2 S60441	hypothetical prote
9	76	8.9	195	2 S42632	ureidoglycolate hy
10	75.5	8.9	336	2 S42632	Flt-15 protein pre
11	75.5	8.9	406	2 T28957	hypothetical prote
12	75.5	8.9	1206	2 S24407	formin isoform IV
13	75	8.8	321	2 T46352	hypothetical prote
14	74.5	8.8	286	2 F82881	hypothetical prote
15	74.5	8.8	482	2 S41211	hypothetical prote
16	74.5	8.8	789	2 S44759	C14B9.5 protein -
17	74.5	8.8	848	2 T00372	hypothetical prote
18	74	8.7	440	2 T47906	FUSCA PROTEIN FUS6
19	74	8.7	953	2 I48078	CHO1 antigen - Chi
20	74	8.7	2197	2 B16000	variant-specific s
21	73.5	8.6	162	2 I49124	interleukin-15 - m
22	73.5	8.6	447	2 S39316	CAB3 protein - hu
23	73.5	8.6	472	2 I59087	ISG-K54 - human
24	73.5	8.6	477	2 S21049	calcium channel pr
25	73.5	8.6	484	2 S39315	CAB3a protein - hu
26	73.5	8.6	484	2 A46608	voltage-dependent
27	73.5	8.6	565	2 G89878	conserved hypotet
28	73.5	8.6	868	2 T31527	hypothetical prote
29	73.5	8.6	2118	2 T13612	hypothetical prote

30	73	8.6	234	2 G97966	hypothetical prote
31	73	8.6	304	2 A32108	transactin initia
32	73	8.6	1291	2 T22282	hypothetical prote
33	72.5	8.5	309	2 T41889	P58 ori153 - Bomb
34	72.5	8.5	380	2 T25454	hypothetical prote
35	72.5	8.5	667	2 D96923	uncharacterized co
36	72.5	8.5	1101	2 T26919	hypothetical prote
37	72	8.5	257	2 C69230	conserved hypotet
38	72	8.5	262	2 F72858	probable methyl tr
39	72	8.5	262	2 T41813	AcMNPV orf69 - Bom
40	72	8.5	546	2 G72210	hypothetical prote
41	72	8.5	719	2 T27977	lin-15A protein -
42	72	8.5	990	2 T43445	hypothetical prote
43	71.5	8.4	421	2 C84555	hypothetical prote
44	71.5	8.4	484	2 S62185	calcium channel be
45	71.5	8.4	674	2 S61181	hypothetical prote

ALIGNMENTS

RESULT 1
A53484
interleukin-15 precursor - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A53484
R:Grabstein, K.H.; Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fung, V.; Bee,
J.; Girdl, J.G.
Science 264, 965-968, 1994
A>Title: Cloning of a T cell growth factor that interacts with the beta chain of the int.
A/Reference number: A53484; MUID:94233380; PMID:8178155
A/Accession: A53484
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-162 <GBA>
A/Cross-references: UNIPROT:P40221; UNIPARC:UPI0000031AC6; GB:U03099; NID:G493521; PIDN:
F:49-162/Product: interleukin-15 #status predicted <MAR>
F:83-133,90-136/Disulfide bonds: #status predicted

Query Match 11.1%; Score 94.5; DB 1; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.19; 48; Indels 15; Gaps 5;
Matches 30; Conservative 23; Mismatches

Qy 43 IDIDOLKNYNDLVPEF-----LPAPEDVETNCWMSAFSCF---OKAQLKSANTGNNE 93
Db 51 VNVISDLKK-IEDILQSMHIDATLYTESDVHPSCKVTAMKCFLELOVISHSQDTIDHD 109

Qy 94 RIINVSIRKLRKRPSTNAGRRQRHRLTSPSCDSYEKKPKPEFLERFKSLQKMH 149
Db 110 TVENLII--LANNLSSNGNTES---GCKKCELEENKRIEFQSFVHIQWFMIN 160

RESULT 2
S29498
lymphocyte antigen ly84 precursor - mouse
C/Alternate names: 38.5K T1 glycoprotein; ST2L protein
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S29498; A33541; S17657; S07054
R:Yanagisawa, K.; Takagi, T.; Tanukamo, T.; Tetsuka, T.; Tomioka, S.
FEBS Lett. 318, 83-87, 1993
A>Title: Presence of a novel primary response gene ST2L, encoding a product highly siml.
A/Reference number: S29498; MUID:33170492; PMID:7916701
A/Accession: S29498
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-567 <YAN>
A/Cross-references: UNIPROT:P14719; UNIPARC:UPI0000029617; EMBL:D13695; NID:G286100; PID:
R:Klemenz, R.; Hoffmann, S.; Werenkiold, A.K.

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Proc. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989
A:Title: Serum- and oncoprotein-mediated induction of a gene with sequence similarity to
A:Reference number: A33541; MUID:89345536; PMID:2527364
A:Accession: A33541
A:Molecule type: mRNA
A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA' <KLE>
A:Cross-references: UNIPARC:UPI000028498; GB:M2484; NID:g201103; PIDN:AAA40160.1; PID:
R:Tomlinaga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.
Biochim. Biophys. Acta 1090, 1-8, 1991
A:Title: Molecular cloning of the murine ST2 gene. Characterization and chromosomal mappe
A:Reference number: S17657; MUID:91355215; PMID:1832015
A:Accession: S17657
A:Molecule type: DNA
A:Status: translation not shown
A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA' <TOM>
A:Cross-references: UNIPARC:UPI000028498; EMBL:X60184; NID:g54200; PIDN:CAA42742.1; PII
R:Tomlinaga, S.I.
FEBS Lett. 258, 301-304, 1989
A:Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells is highly si
A:Reference number: S07054; MUID:90092495; PMID:2532153
A:Accession: S07054
A:Molecule type: mRNA
A:Residues: 1-328, 'SKECPSHIA' <TO2>
A:Cross-references: UNIPARC:UPI000003F02; EMBL:Y07519; NID:g55517; PIDN:CAA68812.1; PIR
A:Note: It is uncertain whether Met-1, Met-7 or Met-19 is the initiator
C:Genetics:
A:Gene: ST2
A:Map position: 1
A:Introns: 27/1; 97/2; 155/3; 210/1; 233/1; 280/2
C:Superfamily: Interleukin-1 receptor type I
C:Keywords: glycoprotein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-337/Product: ST2 protein #status predicted <MAT>
F:60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn) (covalent) #status
Query Match 10.8%; Score 91.5; DB 2; Length 567;
Best Local Similarity 25.6%; Pred. No. 1.3;
Matches 33; Conservative 20; Mismatches 39; Indels 37; Gaps 7;
OY 47 DOLKNYVNDLPEFLPAEDVETNCESWAFSCFOKAOLKSANTGNERIINVSIIKGLRK 106
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 DRLK-----FLPAFVE-----DSGIYACV-----IRSPNL-NKTGYLWVTIHK--K 113
OY 107 PPSTN-----AGRQKHRLTPESCDSEYKKPKPEFLEPKSLLOKWIHQH----- 151
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 PPSCIPIDPLYMSTVGRGSKNFKITCPTIDLYNMTAPVQWPKCKALQEPFRFRAHSYLF 173
OY 152 LSSRTGSE 160
: : |||
Db 174 IDNTHDDE 182

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[illegible]

Db 132 RDENHTSIKPEPEETCKLLEKHPDDLISAFIHESARHNPDIYPAAVIALTQYHKLAEHC 191
Qy 125 CDSYKKPKPEFLERFKSLQKMIHQHLSRTGSED 161
Db 192 CEEEDKE--KCFSEKMKQLMK-----QSHSIED 217

RESULT 5

S49882
hypothetical protein YJL127C - Yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein Y18277.02c
C/Species: Saccharomyces cerevisiae
C/Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S49882
R/Hamlyn, N.; Church, C.
submitted to the EMBL Data Library, November 1994
A/Reference number: S49881
A/Accession: S49882
A/Molecule type: DNA
A/Residues: 1-206 <HAM>
A/Cross-references: UNIPROT:P40470; UNIPARC:UPI000013B441; GB:Z47047; EMBL:Z46833; NID:G
C/Genetics:
A:Gene: MIPS:YJL127C
A/Cross-references: SGD:S0001389
A/Map position: 9L

Query Match 9.3%; Score 79; DB 2; Length 206;
Best Local Similarity 26.1%; Pred. No. 6.4;
Matches 29; Conservative 18; Mismatches 48; Indels 16; Gaps 3;

Qy 48 QLNKYVNDLVPEFLPAPEDVETNCMSAFSCFOQAOLKSANTGNRRINVSICKLRKP 107
Db 12 QATSVVNGLLSNLPGPKIRANNGKTSVNNGSKAQLIDRLKKRVQQLQNRDVHKIKKCC 71

Qy 108 PSTNAGRRQKRLTCLPCSDSYKKPKPEFLERF--KSLIQKMIHQHLSRT 156
Db 72 KLVKKKKVKQKHL-----DKQLQLAKHGVLR--HQHEGLT 108

RESULT 6

JC7822
isocitrate dehydrogenase (NADP) (EC 1.1.1.42), monomeric type - Azotobacter vinelandii
C/Species: Azotobacter vinelandii
C/Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
C/Accession: JC7822; PC7187
R/Sahara, T.; Takeuchi, Y.; Yamaoka, N.; Fukunaga, N.
BioSci. Biotechnol. Biochem. 66, 489-500, 2002
A/Title: Cloning, sequencing, and expression of a gene encoding the monomeric isocitrate
A/Reference number: JC7822; PMID:12005040; MUID:21999801
A/Accession: JC7822
A/Molecule type: DNA
A/Residues: 1-741 <SAH>
A/Cross-references: UNIPROT:P16100; UNIPARC:UPI000012D1CA; DDBJ:D73443

A/Accession: PC7187
A/Molecule type: Protein
A/Residues: 2-16 <SA2>
A/Cross-references: UNIPARC:UPI000017GDF5
C/Comment: This enzyme that catalyzes the oxidative decarboxylation of isocitrate to alpha
his bacterium is typical mesophilic, it contributes to the respiratory protection of nit
C/Genetics:
A:Gene: icd
C/Superfamily: isocitrate dehydrogenase, monomeric type
C/Keywords: oxidoreductase

Query Match 9.2%; Score 78; DB 2; Length 741;
Best Local Similarity 24.8%; Pred. No. 31;
Matches 26; Conservative 23; Mismatches 34; Indels 22; Gaps 4;

Qy 33 DRHMRKRLIDVIDQLKNYVNDL-----VPEFLPAPEDVETNCMSAFSCFOQAOLKS 86
Db 77 DANIKLPNISASVPLKAKKEIQGGCYKLPDI---PEEKPTDEKDVKARYKIKGSA 133

Qy 87 AN-----TGNNRRINVSICKLRKPSTNAGRRQKRLTCLPCSDS 127
Db 134 VNPVLRGNSDRRAPLSVKYARKHP-----HGMGMSADS 169

RESULT 7

A25876
vitellogenin III precursor - fruit fly (Drosophila melanogaster)
N/Alternate names: yolk polypeptide yP11; yolk protein 3
C/Species: Drosophila melanogaster
C/Date: 04-Mar-1988 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C/Accession: A25876; A27388
R/Yan, Y.L.; Kunert, C.J.; Postlethwait, J.H.
Nucleic Acids Res. 15, 67-85, 1987
A/Title: Sequence homologies among the three yolk polypeptide (Yp) genes in Drosophila m

A/Reference number: A25876; MUID:87146365; PMID:3029679
A/Accession: A25876
A/Molecule type: DNA
A/Residues: 1-420 <YAN>
A/Cross-references: UNIPROT:P06607; UNIPARC:UPI0000080099; GB:X04754; NID:G8844; PIDN:CA
R/Garabedian, M.J.; Shitras, A.D.; Bowmer, M.; Mensink, P.C.
Gene 55, 1-8, 1987
A/Title: The nucleotide sequence of the gene coding for Drosophila melanogaster yolk pro

A/Reference number: A27388; MUID:87305580; PMID:3114046
A/Accession: A27388
A/Molecule type: DNA
A/Residues: 1-420 <GAR>
A/Cross-references: UNIPARC:UPI0000080099; GB:M1898; NID:G158815; PIDN:AAA29024.1; PID:
C/Genetics:
A:Gene: FlyBase:Yp3
A/Cross-references: FlyBase:FBgn0004047
C/Superfamily: insect vitellogenin
C/Keywords: egg yolk; glycoprotein; phosphoprotein; sulfoprotein
F,1-19/Domain: signal sequence #status predicted <SIG>

Query Match 9.0%; Score 76.5; DB 2; Length 420;
Best Local Similarity 24.4%; Pred. No. 23;
Matches 39; Conservative 14; Mismatches 54; Indels 53; Gaps 7;

Qy 8 MERIVCLMWIFLGTIVHKSSSGQDR-----HMIRQLIDI----- 45
Db 1 MMSLRICLATCLVAHAKSDASNDRLKPTKMLTATELEVPISINDITWERLENOPLQ 60

Qy 46 -----VDQKNYVNDLVPEFLPAPEDVETNCMSAFSCFOQAOLK-----SA 87
Db 61 GAKVIEKIVHGQIR--HDLTPSFVPSFNPV--WIKSNQKVECKLNNYETAKA 114

Qy 88 NTGNNRRINVSICKL-KRKPPSTNAGR-----QKRL 120
Db 115 QPFGEDVETIVLTGLPKTSBAQKAKRRLIQAVYQKYNL 154

RESULT 8

S60441
hypothetical protein YGR150C - Yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein G6642
C/Species: Saccharomyces cerevisiae
C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S60441; S64459
R/Skala, J.; Nawrocki, A.; Goffeau, A.
Yeast 11, 1421-1427, 1995
A/Title: The sequence of a 27 kb segment on the right arm of chromosome VII from Sacchar

A/Reference number: S60435; MUID:96158062; PMID:8585325
A/Accession: S60441

A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-864 <SKA>

A/Cross-references: UNIPROT:P48237; UNIPARC:UPI000005309F; EMBL:X85807; NID:G1045249; PI
R/Van Dyck, L.; Skala, J.; de Wierfossse, P.; Purnelle, B.; Talia, E.; Nawrocki, A.; Del
submitted to the Protein Sequence Database, May 1996
A/Reference number: S64458
A/Accession: S64459

A:Molecule type: DNA
A:Residues: 1-864 <VAN>
A:Cross-references: UNIPARC:UPI000005309F; EMBL:Z72935; NID:g1323253; PIDN:CAA97164.1; F
A:Experimental source: strain S288C
C:Genetics:
A:Cross-references: SGD:S0003382
A:Map position: 7R

Query Match 9.0%; Score 76.5; DB 2; Length 864;
Best Local Similarity 22.5%; Pred. No. 49;

Matches 43; Conservative 22; Mismatches 59; Indels 67; Gaps 8;

QY 2 RSSPGRNRYIYC---LMVFLGLTVHKSSQGDRIIMRQIDIVDQLKQYVNDLV 57
DB 5 RCGPKNM---VLCFPFQUSFLFSKRLNK-----RKYTLQTEDE-KMMWSLS 49
QY 58 PEFLPADEVETNCWSAFSCFOKAOLKSANTGNMERIINVSIKLKKRPSTNAGRQK 117
DB 50 KKKITPEDEV-----FKLAQLREFSNTLKERIHNTK-----SVNSDGHQS 90
QY 118 HRLTSPSCDYEKKPKP-----EFLERFKSLLOKMIHQ----- 150
DB 91 NSIAPISDESRNVAVTTSVYPNEEKSNDLSLIHSFLEKMDHLVPKIVRERVAADDIL 150
QY 151 --HLSRTHGS 159
DB 151 AKNLPRSHSN 161

RESULT 9
S42022
ureidoglycolate hydrolase (EC 3.5.3.19) - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein YIR032C
C/Species: Saccharomyces cerevisiae
C/Date: 31-Mar-1992 #sequence_revision 14-Sep-1994 #text_change 05-Oct-2004
C/Accession: S42022; S48494
R/Yeo, H.S.; Cooper, T.G.
Yeast 7, 693-698, 1991
A>Title: The ureidoglycolate hydrolase (DAL3) gene in Saccharomyces cerevisiae.
A/Reference number: S42022; MUID:92133160; PMID:1776360
A:Molecule type: DNA
A:Residues: 1-195 <YOO>
A:Cross-references: UNIPROT:P32459; UNIPARC:UPI00000529B; EMBL:M64778; NID:g171369; PID
R/Rowley, K.
submitted to the EMBL Data Library, October 1994
A/Reference number: S48494
A:Accession: S48494
A:Molecule type: DNA
A:Residues: 1-195 <ROM>
A:Cross-references: UNIPARC:UPI00000529B; GB:Z47047; EMBL:Z38061; NID:g603997; PID:g763
C/Genetics:
A:Gene: SGD:DAL3
A:Cross-references: SGD:S0001471; MIPS:YIR032C
A:Map position: 9R
C:Superfamily: ureidoglycolate hydrolase
C/Keywords: allantoin degradation; hydrolase; lipoprotein; methylated carboxyl end; pre
F/192/Binding site: larnesyl (Cys) (covalent) #status predicted
F/192/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match 8.9%; Score 76; DB 2; Length 195;
Best Local Similarity 27.6%; Pred. No. 11;
Matches 24; Conservative 14; Mismatches 29; Indels 20; Gaps 3;

QY 24 VHKSSGQDRHIMRQIDIVDQLKQYVNDLVPEFLPADEVETNCWSAFSCFOKAQ 83
DB 33 LEKGANGGT---AIKLLQ---VSQVENKSKTSKVP-----NMNLFPCFPQPH 72
QY 84 LKSANTGNMERIINVSIKLKKRPST 110
DB 73 LNRVFTGSGNOAISHSIKVLEKHPGST 99

RESULT 10

S42632
Fit-1S protein precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S42632
R/Bergers, G.; Reikertorfer, A.; Braselmann, S.; Gruninger, P.; Bueslinger, M.
EMBO J. 13, 1176-1188, 1994
A>Title: Alternative promoter usage of the Fos-responsive gene Fit-1 generates mRNA isofo
A/Reference number: S42632; MUID:94178260; PMID:8131748
A:Accession: S42632
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <BER>
A:Cross-references: UNIPROT:Q62611; UNIPARC:UPI000002AC15; GB:U04319; NID:g488278; PIDN:
C:Superfamily: vaccinia virus B15R protein; Immunoglobulin homology

Query Match 8.9%; Score 75.5; DB 2; Length 336;
Best Local Similarity 22.2%; Pred. No. 23;
Matches 30; Conservative 26; Mismatches 42; Indels 37; Gaps 6;

QY 43 IDIVDQLKQYVNDLV-----EFLPADEVETNCWSAFSCFOKAOLKSAN 88
DB 49 INPEWYYSNTNERIPQKRNRIFVSRDLKFLPAKVE-----DSGIYTCVIRSP-ESIK 102
QY 89 TGNMERIINVSIKLKKRP-----STNAGRQKRLTGPCSDSYEKKRPKEFLE 138
DB 103 TGS---LNVITLYK---RPNCKIPDYMYSTVDGSDKSKITCPTALYNMTAPVOMFK 155
QY 139 RPKSLQKMIHQHLS 153
DB 156 NCKALQGRPRRAHWS 170

RESULT 11

T28957
hypothetical protein F45F2.11 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T28957
R/Davidson, S.; Woldmann, P.
submitted to the EMBL Data Library, July 1996
A>Description: The sequence of C. elegans cosmid F45F2.
A/Reference number: Z20548
A:Accession: T28957
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-406 <DAV>
A:Cross-references: UNIPROT:Q22975; UNIPARC:UPI00000765A; EMBL:U64845; PIDN:AAC48032.1;
A:Experimental source: strain Bristol N2; clone F45F2
C/Genetics:
A:Gene: CESP:F45F2.11
A:Map position: 5
A:Insertions: 1/2; 24/2; 143/3; 307/2; 338/2

Query Match 8.9%; Score 75.5; DB 2; Length 406;
Best Local Similarity 20.5%; Pred. No. 28;
Matches 38; Conservative 23; Mismatches 55; Indels 69; Gaps 7;

QY 26 KSSSGQDRHIMRQIDIVDQLKQYVNDLVPEFLP----- 62
DB 13 KSSPQSDENFPKRLQWCKRLRLK-----TEPFLSESELLEIKNEKSGIOKGENEG 66
QY 63 -----APDEVETNCW-----SAFSCFOKAOLKSANTGNER 94
DB 67 ENEKCEFRPVVTPNEIDSHKEWYHRLMLKLYKGERGAPFPFPPPLPSMMIAASNA 126
QY 95 IINVSIKLKR-----KPSSTNAGRQKRLTGPCSDSYEKKRPKEFLERFKSLQKM 147
DB 127 VSFNAFDEVRAAQAATAKSPSTSLERRAQR-CPA-DFQPLPPPHITILEMTTLAP-- 182
QY 148 IHQHL 152

Db 183 -HOXI 186

RESULT 12

S24407

formin isoform IV - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S24407

R:Jackson-Grusby, L.; Kuo, A.; Leder, P.

Genes Dev. 6, 29-37, 1992

A:Title: A variant limb deformity transcript expressed in the embryonic mouse limb defect

A:Reference number: S24407; MUID:92112033; PMID:1339380

A:Accession: S24407

A:Molecule type: mRNA

A:Residues: 1-1206 <AAC>

A:Cross-references: UNIPROT:Q05859; UNIPARC:UPI0000027920; EMBL:X62379; NID:g51552; PIDN

Query Match 8.8%; Score 75.5; DB 2; Length 1206;

Best Local Similarity 22.0%; Pred. No. 86;

Matches 37; Conservative 41; Mismatches 69; Indels 21; Gaps 8;

2 RSSPG-NMERI-VICLMVIFGLTVHKSSSQGQ-DEHMTIRMQLDIVDQKLVYV-- 54

953 RASGGLHMSVXQDILALITLFGNYMNGNRTGQADGYSLEILPKDKDVSRDNGMLV 1012

55 DLVEFLPAPDEVETNCESAFSCFOKAQLKSANTGNRIINVSIKKLKRPSTNAGR 114

1013 DYVVKYLYRYVDQEGAGTDSVFPLEPQDFLASQVKEFDLLK-DLRKLKQLEAS---- 1067

115 RQKRLTGPCSDSYEKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

1068 EQQKLVLC-----KESPREYLOPFKDKLEFFKK-AKKEHKMEES 1106

Db

Query 13

T46352

hypothetical protein DKFZp434C0816.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T46352

A:Reference number: 223037

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-321 <AAA>

A:Cross-references: UNIPROT:Q9UIC8; UNIPARC:UPI000016ACAD; EMBL:AL137283

A:Experimental source: adult testis; clone DKFZp434C0816

C:Genetics:

A:Note: DKFZp434C0816.1

Query Match 8.8%; Score 75; DB 2; Length 321;

Best Local Similarity 23.0%; Pred. No. 24;

Matches 42; Conservative 29; Mismatches 64; Indels 48; Gaps 10;

24 VHKSSSQGQDRHMT-----RMROLIDIVDQKN-YVNDLVPEFLPA-----P 64

134 LHSDDTLQMDHIDLSKRYAVIGADLRSLSEELKKCNNTQQLPTLLIECVLVYWP 193

65 EDVETNCESAFSCFOKAQL--KSANTGNRIINVSIKKLKRP-----PSTNAGR 115

194 EQSANLTKMANNS-FERAMFINVEQVNG--DRFGQIMIENTLRRRCOLAGVETCKSL 250

116 QKHL-----TCSCDSYE--KKPK-----ELERFKSLLOKMIHQHLSRTHG 158

251 QKERLISNGWETASAVDMELYNRLPRAEVSRIESLEFLDEMBELLOLMRHYCLCWATKG 310

Query 159 SED 161

Db 311 GNE 313

RESULT 14

F82881

hypothetical protein U0505 (imported) - Ureaplasma urealyticum

C:Species: Ureaplasma urealyticum

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: F82881

R:Glass, J.I.; Letkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to Genbank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min

A:Reference number: A82870

A:Accession: F82881

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <GLA>

A:Cross-references: UNIPARC:UPI00000C1C9A; GB:AE002149; GB:AF222894; NID:g6899503; PIDN:

A:Experimental source: serovar 3; biovar 1

C:Genetics:

A:Gene: U0505

A:Genetic code: SGC3

Query Match 8.8%; Score 74.5; DB 2; Length 286;

Best Local Similarity 20.6%; Pred. No. 24;

Matches 42; Conservative 38; Mismatches 59; Indels 65; Gaps 9;

6 GNMRIYICLMVIFGLTVHKSS-----SSQGDHMMIRMQLDIVD 47

21 GGIISLIVITVAILGVILSTQNTNKSKEPLTOIEDNINNKQDAH--KVNENITIID 78

48 QLK-----NVVN--DLVEFLPAPDEVETNCESAFSCFOKAQLKSANTGN 92

79 KKGIIHKKIDITKINOQKEILKDKLKKKEK-----NKDQINNTNEVLN 126

93 ERIINV-----SIKKLKRKPSTNAGRQKRLTGPCSDSYEKPKPEFLERPKS 142

127 KPIINVKVDDKKNQKQENSTKLKNNDFISNNDKNNK--INENNNISYEKPKPK--LKRENI 182

Db

Query 143 L-----LOKMIHQHLSRTHGSEDS 162

183 INVIAKKMDLYQLDFTYFSNEN 206

Db

RESULT 15

S41211

voltage-dependent calcium channel protein - human

C:Species: Homo sapiens (man)

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C:Accession: S41211

R:Collin, T.; Lory, P.; Taviaux, S.; Courtieu, C.; Guibault, P.; Berta, P.; Nargeot, J.

Eur. J. Biochem. 220, 257-262, 1994

A:Title: Cloning, chromosomal location and functional expression of the human voltage-de-

A:Reference number: S41211; MUID:94164167; PMID:8119293

A:Accession: S41211

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-482 <COL>

A:Cross-references: UNIPROT:P54284; UNIPARC:UPI0000160BD2; GB:L27584; NID:g443663; PIDN:

C:Superfamily: human voltage-dependent calcium channel beta chain

Query Match 8.8%; Score 74.5; DB 2; Length 482;

Best Local Similarity 20.8%; Pred. No. 41;

Matches 36; Conservative 27; Mismatches 65; Indels 45; Gaps 7;

9 ERIYICLMVIFGLTVHKSSSQGQDRHMMIRMQLDIVDQKN--YVNDLVPE-----FL 61

59 EAFVIRNVISYGLVDECPQSGVN-FAKADPLHKEXYSNMWIGRLVKEGGDLAFI 117

62 PAVEDVETNCESAFSCFOKAQLKSANTGNRIINVSIKKLKRPSTNAGRQKRL-- 119

118 PSPQRL-----SIRLQEQKARSGNPSISDIG--NRRSPPSLKKOKQKQAEH 166

Db

Query 120 -----LTCPSCDSYEKPKPEFLERFKSLLOKMIHQHLSRTHG 158

Thu Sep 7 14:13:59 2006

us-10-659-684-2.rpr

Page 6

Db 167 VPPYDVVPSMRPVVLVGPSLKGYE-----VTDMMQKALPDLKHRFDG 209

Search completed: September 7, 2006, 12:52:26
Job time : 14.8029 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:40:11 ; Search time 89.3314 Seconds
(without alignments)
1677.489 Million cell updates/sec

Title: US-10-659-684-2

Perfect score: 850
Sequence: 1 MRSSPGNMERIVICLWVIFL.....LLOKMHQHLSTRTGSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	95.6	155	1121_HUMAN	Q9bhe4 homo sapien
2	629	74.0	146	1121_BOVIN	Q761u5 bos taurus
3	609	71.6	146	1121_PIG	Q761u5 sus scrofa
4	604	71.1	146	1121_CANFA	Q61719 canis famli
5	486	57.2	146	1121_MOUSE	Q6e617 mus musculu
6	486	57.2	146	Q5SUE2_MOUSE	Q5eue2 mus musculu
7	392	46.1	123	1121_PERRA	Q80xg2 peromyscus
8	171.5	20.2	145	Q58106_CHICK	Q581u6 gallus galli
9	119.5	14.1	145	Q38121_TETNG	Q38121 tetradon n
10	106.5	12.5	162	1115_FELCA	Q97687 felis silve
11	99.5	11.7	135	Q6FEG7_HUMAN	Q6feg7 homo sapien
12	99.5	11.7	162	1115_HUMAN	P40933 homo sapien
13	99.5	11.7	162	Q49528_HUMAN	Q49528 homo sapien
14	98.5	11.6	155	Q59902_FUGRU	Q599u2 tingu rubrip
15	98.5	11.6	162	1115_RABIT	Q35758 oryctolagus
16	98	11.5	162	Q5W7F5_BRARE	Q5w7f5 brachydantio
17	96	11.3	160	Q32PM5_BRARE	Q32pm5 brachydantio
18	94.5	11.1	162	1115_CERRA	P40221 ceropithec
19	94.5	11.1	162	1115_MACMU	P48092 macaca mulia
20	94.5	11.1	162	Q4U002_MACTH	Q4u0u2 macaca thib
21	92	10.8	163	Q2PUG6_RABIT	Q2pug6 oryctolagus
22	91.5	10.8	337	Q5D095_MOUSE	Q5d095 mus musculu
23	91.5	10.8	567	11R11_MOUSE	P14779 mus musculu
24	91.5	10.8	567	Q3UM53_MOUSE	Q3um53 mus musculu
25	90.5	10.6	162	1115_BOVIN	Q30u28 bos taurus
26	90.5	10.6	162	1115_SHEEP	Q9x616 ovis aries
27	89.5	10.5	162	Q75S29_CAVPO	Q75s29 capra porce
28	87.5	10.3	162	Q6B416_HORSE	Q6b416 equus cabal
29	86.5	10.2	162	Q5E8K6_MARMO	Q5e8k6 marmota mon
30	86.5	10.2	722	Q7MDK0_VIBVY	Q7mdk0 vibrio vuln
31	86	10.1	466	Q5C0J3_SCHUA	Q5c0j3 schistosoma

32	85.5	10.1	105	2	Q5W7F6_BRARE	Q5w7f6 brachydantio
33	85.5	10.1	162	2	Q4GZ11_BUBBU	Q4gz11 bubalus bub
34	85.5	10.1	162	2	Q5WQV8_MARMO	Q5wqv8 marmota mon
35	85.5	10.1	278	2	Q4Z302_PLABE	Q4z302 plasmodium
36	85	10.0	311	2	Q81913_LOXLA	Q81913 loxocleas
37	84.5	9.9	511	2	Q5A2U1_CANAL	Q5a2u1 candida alb
38	84.5	9.9	722	2	Q8D6P4_VIBVY	Q8d6p4 vibrio vuln
39	84.5	9.9	1516	2	Q4WQ6_ASPTU	Q4wq6 aspergillus
40	83.5	9.8	582	2	Q8DU56_SYNEU	Q8dus6 synechococ
41	83.5	9.8	3052	2	Q82933_POPTV	Q82933 johnsongras
42	83	9.8	414	2	Q7MNL4_VIBVY	Q7mnl4 vibrio vuln
43	83	9.8	607	2	Q642P7_XENLA	Q642p7 xenopus lae
44	83	9.8	899	2	Q4FIJ3_9ENIR	Q4fij3 salmonella
45	83	9.8	899	2	Q52336_9Z2ZZ	Q52336 plasmid r64

ALIGNMENTS

RESULT 1
ID 1121_HUMAN 1121_HUMAN STANDARD; PRT; 155 AA.
AC Q9HBE4;
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
DT 23-NOV-2004, Sequence version 2.
DT 07-FEB-2006, entry version 24.
DE Interleukin-21 precursor (IL-21) (Za11).
GN Name=IL21;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;
RA Parish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Heipel M., Brandt C., Kuiper J.L., Kramer J., Conklin D., Pressnell S.R., Berry J., Shiota F., Bort S., Hamblly K., Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond P., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kaushansky K., Holly R.D., Foster D.;
RT "Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function.";
RL Nature 408:57-63 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P., Nguyen D.A., Livingston R.J., Poel C.L., Nickerson P.D., Schachwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "Seacalcin, a novel G-protein-coupled receptor for genomic applications, UM-SuMRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg K., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stedman M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toehiyuki S., Carninci P., Prange C., Rana S.S., Luquliano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.K., Mozley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnorch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP FUNCTION.
RX PubMed:15178704; DOI=10.1189/j.1003488;
RA Strenge M., Jalkanen I., Matikainen S.;
RT "IFN- α 1 α regulates IL-21 and IL-21R expression in human NK and T
RL cells.";
RN J. Leukoc. Biol. 76:416-422(2004).
RP REVIEW.
RX PubMed:15147560; DOI=10.1111/j.1365-2567.2004.01886.x;
RA Sivakumar P.V., Foster D.C., Clegg C.H.;
RT "Interleukin-21 is a T-helper cytokine that regulates humoral immunity
RT and cell-mediated anti-tumour responses.";
RL Immunology 112:177-182(2004).
CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
CC transition between innate and adaptive immunity. Induces the
CC production of IgG(1) and IgG(3) in B-cells (By similarity). May
CC play a role in proliferation and maturation of natural killer (NK)
CC cells in synergy with IL15. May regulate proliferation of mature
CC B- and T-cells in response to activating stimuli. In synergy with
CC IL15 and IL18 stimulates interferon gamma production in T-cells
CC and NK cells. During T-cell mediated immune response may inhibit
CC dendritic cells (DC) activation and maturation.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed in activated CD4-positive T-cells
CC but not in CD8-positive T-cells, B-cells, or monocytes.
CC -1- SIMILARITY: Belongs to the IL-21 family.
CC
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CC Distributed under the Creative Commons Attribution-NonDerivative License
CC
DR EMBL: AF254069; AAC29348.1; ALT_INIT; mRNA.
DR EMBL: AY763518; AAU88182.1; ALT_INIT; genomic_DNA.
DR EMBL: BC066258; AAH66258.1; ALT_INIT; mRNA.
DR EMBL: BC066259; AAH66259.1; ALT_INIT; mRNA.
DR EMBL: BC066260; AAH66260.1; ALT_INIT; mRNA.
DR EMBL: BC066261; AAH66261.1; ALT_INIT; mRNA.
DR EMBL: BC066262; AAH66262.1; ALT_INIT; mRNA.
DR EMBL: BC069124; AAH69124.1; ALT_INIT; mRNA.
DR EMBL: ENSG00000138664; Homo sapiens.
DR HGN: HGNC:6005; IL21.
DR MIM: 605384; gene.
DR GO: GO:0005615; C:extracellular space; NAS.
DR GO: GO:0005134; F:interleukin-2 receptor binding; IPI.
DR GO: GO:0048469; P:cell maturation; IDA.
DR GO: GO:0045078; P:positive regulation of interferon-gamma bio. .; NAS.
DR GO: GO:0042102; P:positive regulation of T cell proliferation; IDA.
DR GO: GO:0007165; P:signal transduction; NAS.
KM Cytokine; Glycoprotein; Signal.
FT CHAIN 1 22 Potential.
FT CHAIN 23 155 Interleukin-21.
FT CARBOHYD 90 90 /FtId=PRO_0000015505.
FT DISULFID 64 115 N-linked (GlcNAc...) (Potential).
FT DISULFID 71 118 Potential.
SQ SEQUENCE 155 AA; 17923 MW; E994A3D19029B914 CRC64;
Query Match 95.6%; Score 813; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.8e-64;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 128 YEKPPKEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db 121 YEKPPKEFLERFKSLQKMIHQHLSRTHGSEDS 155
RESULT 2
ID IL21 BOVIN STANDARD; PRT; 146 AA.
AC Q76LU5;
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
DT 23-NOV-2004, sequence version 2.
DT 07-FEB-2006, entry version 12.
DE Interleukin-21 precursor (IL-21).
GN Name:IL21;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], PROTEIN SEQUENCE OF 18-32, SUBCELLULAR
RP LOCATION, AND TISSUE SPECIFICITY.
RX PubMed:12963638; DOI=10.1016/S0165-2427(03)00106-5;
RA Muneta Y., Kikuna R., Yoshihara K., Mori Y.;
RT "Cloning, expression, and tissue distribution of bovine interleukin-
RT 21.";
RL Vet. Immunol. Immunopathol. 95:73-80(2003).
CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
CC transition between innate and adaptive immunity. Induces the
CC production of IgG(1) and IgG(3) in B-cells. May play a role in
CC proliferation and maturation of natural killer (NK) cells in
CC synergy with IL15. May regulate proliferation of mature B- and T-
CC cells in response to activating stimuli. In synergy with IL15 and
CC IL18 stimulates interferon gamma production in T-cells and NK
CC cells (By similarity). During T-cell mediated immune response may
CC inhibit dendritic cells (DC) activation and maturation (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed in spleen, but not in the brain,
CC heart, kidney, liver, and lung.
CC -1- SIMILARITY: Belongs to the IL-21 family.
CC
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CC Distributed under the Creative Commons Attribution-NonDerivative License
CC
DR EMBL: AB073021; BAC87747.1; ALT_INIT; mRNA.
DR EMBL: BC066258; AAH66258.1; ALT_INIT; mRNA.
DR EMBL: BC066259; AAH66259.1; ALT_INIT; mRNA.
DR EMBL: BC066260; AAH66260.1; ALT_INIT; mRNA.
DR EMBL: BC066261; AAH66261.1; ALT_INIT; mRNA.
DR EMBL: BC066262; AAH66262.1; ALT_INIT; mRNA.
DR EMBL: BC069124; AAH69124.1; ALT_INIT; mRNA.
DR EMBL: ENSG00000138664; Homo sapiens.
DR HGN: HGNC:6005; IL21.
DR MIM: 605384; gene.
DR GO: GO:0005615; C:extracellular space; NAS.
DR GO: GO:0005134; F:interleukin-2 receptor binding; IPI.
DR GO: GO:0048469; P:cell maturation; IDA.
DR GO: GO:0045078; P:positive regulation of interferon-gamma bio. .; NAS.
DR GO: GO:0042102; P:positive regulation of T cell proliferation; IDA.
DR GO: GO:0007165; P:signal transduction; NAS.
KM Cytokine; Direct protein sequencing; Signal.
FT CHAIN 1 17 Probable.
FT CHAIN 18 146 Interleukin-21.
FT DISULFID 64 115 /FtId=PRO_0000015503.
FT DISULFID 71 118 Potential.
SQ SEQUENCE 146 AA; 16948 MW; 696566DA73F4B8BC CRC64;
Query Match 74.0%; Score 629; DB 1; Length 146;
Best Local Similarity 81.5%; Pred. No. 4.4e-48;
Matches 119; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Oy 8 MERIVICLAWIFLGTLVHKSSGQODRHIMRMROLIDIVDQKXVNDLVPEFLPAPEDV 67
Db 1 MERIVICLAWIFLGTLVHKSSGQODRHIMRMROLIDIVDQKXVNDLVPEFLPAPEDV 60
Oy 68 ETNCWMSAFSCFOKAQLKSANTGNNERIINVSIKLKRKPPSTNAGRGRLTGPCSDS 127
Db 61 KRHCERSAFSCFOKAQLKSANTGNNERIINVSIKLKRKPPSTNAGRGRLTGPCSDS 120
Oy 128 YEKPPKEFLERFKSLQKMIHQHLS 153
Db 121 YEKPPKEFLERFKSLQKMIHQHLS 146
RESULT 3

IL21_PIG STANDARD; PRT: 146 AA.
 AC Q76LUG;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 23-NOV-2004, sequence version 2.
 DE Interleukin-21 precursor (IL-21).
 GN Name=IL21;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
 OC Sus.
 NCBI_TaxID=96823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND SUBCELLULAR LOCATION.
 RX PubMed:15107555; DOI=10.1292/jvms.66.269;
 RA Muneta Y., Kikuma R., Uenishi H., Hoshino T., Yoshihara K., Tanaka M.,
 RA Hanashima N., Mori Y.;
 RT "Molecular cloning, expression and biological function of porcine
 RT interleukin-21.";
 RL J. Vet. Med. Sci. 66:269-275(2004).
 CC -I- FUNCTION: Cytokine with immunoregulatory activity. May promote the
 CC transition between innate and adaptive immunity. Induces the
 CC production of IgG(1) and IgG(3) in B-cells. May play a role in
 CC proliferation and maturation of natural killer (NK) cells in
 CC synergy with IL15. May regulate proliferation of mature B- and T-
 CC cells in response to activating stimuli. In synergy with IL15 and
 CC IL18 stimulates interferon gamma production in T-cells and NK
 CC cells (By similarity). During T-cell mediated immune response may
 CC inhibit dendritic cells (DC) activation and maturation.
 CC -I- SUBCELLULAR LOCATION: Secreted protein.
 CC -I- SIMILARITY: Belongs to the IL-21 family.
 CC
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC
 DR EMBL, AB073020; BAD11128.1; ALT_INIT; mRNA.
 KW Cytokine; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 146 Interleukin-21.
 FT DISULFID 64 115 /FTID=PRO_0000015508.
 FT DISULFID 71 118 Potential.
 SQ SEQUENCE 146 AA; 16833 MW; 835C63B716230BD1 CRC64;
 Query March 71.6%; Score 609; DB 1; Length 146;
 Best Local Similarity 80.1%; Pred. No. 2,7e-46;
 Matches 117; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 8 MERIVICIMVIFLGTLVHKSSSGQDRHIMRQLIDIVDQKNVNDLVEFLPAPBDV 67
 DB 1 MEKIVICIMVIFSGTVAHKSSFGQDRLIRLRQIDIVDQKNVNDLVEFLPAPBDV 60
 QY 68 ETNCEWSAFSCFOKAQLKSAANTGNERRIINVSIKLKRKPSTNAGRQKRLTSPSCDS 127
 DB 61 QRHCESAFSCFOKVELKSANTGNEKIINVLTKRKLPPTNAGRRQKRLTSPSCDS 120
 QY 128 YEKRPKEFLERFKSLQKMIHQLS 153
 DB 121 YEKRPKEFLERFKSLQKMIHQLS 146

RESULT 4
 IL21_CANFA STANDARD; PRT: 146 AA.
 AC Q6L7I9;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Interleukin-21 precursor (IL-21).
 GN Name=IL21;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC Tissue=Spleen;
 RA Miyake M., Saze K., Haga Y., Yamamoto Y., Iwabuchi S.;
 RT "Molecular cloning of canine interleukin-21 cDNA.";
 RL Submitted (DSC-2003) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: Cytokine with immunoregulatory activity. May promote the
 CC transition between innate and adaptive immunity. Induces the
 CC production of IgG(1) and IgG(3) in B-cells. May play a role in
 CC proliferation and maturation of natural killer (NK) cells in
 CC synergy with IL15. May regulate proliferation of mature B- and T-
 CC cells in response to activating stimuli. In synergy with IL15 and
 CC IL18 stimulates interferon gamma production in T-cells and NK
 CC cells (By similarity). During T-cell mediated immune response may
 CC inhibit dendritic cells (DC) activation and maturation (By
 CC similarity).
 CC -I- SUBCELLULAR LOCATION: Secreted protein (By similarity).
 CC -I- SIMILARITY: Belongs to the IL-21 family.
 CC
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 CC
 DR EMBL, AB127975; BAD22569.1; - mRNA.
 DR Ensembl; ENSCAFG0000004004; Canis familiaris.
 KW Cytokine; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 146 Interleukin-21.
 FT DISULFID 64 115 /FTID=PRO_0000015504.
 FT DISULFID 71 118 Potential.
 SQ SEQUENCE 146 AA; 16776 MW; FFE8DF836AF219AA CRC64;
 Query March 71.1%; Score 604; DB 1; Length 146;
 Best Local Similarity 80.8%; Pred. No. 7.4e-46;
 Matches 118; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 8 MERIVICIMVIFLGTLVHKSSSGQDRHIMRQLIDIVDQKNVNDLVEFLPAPBDV 67
 DB 1 MEKIVICIMVIFSGTVAHKSSFGQDRLIRLRQIDIVDQKNVNDLVEFLPAPBDV 60
 QY 68 ETNCEWSAFSCFOKAQLKSAANTGNERRIINVSIKLKRKPSTNAGRQKRLTSPSCDS 127
 DB 61 KRHCESAFSCFOKVELKSANTGNEKIINVLTKRKLPPTNAGRRQKRLTSPSCDS 120
 QY 128 YEKRPKEFLERFKSLQKMIHQLS 153
 DB 121 YEKRPKEFLERFKSLQKMIHQLS 146

RESULT 5
 IL21_MOUSE STANDARD; PRT: 146 AA.
 AC Q9S8I7;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2001, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE Interleukin-21 precursor (IL-21).
 GN Name=IL21;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=BALB/c;
 RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;
 RA Parfieb-Novak J., Dillon S.R., Nelson A., Sprecher C.,
 RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader C.,
 RA Burkhead S., Heipel M., Brandt C., Kujper J.L., Kramer J.,

RA Conklin D., Prensell S.R., Berry J., Shiota F., Bort S., Hamblly K.,
RA Modiri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer W., Kaushansky K., Holly R.D., Foster D.;
RT "Interleukin 21 and its receptor are involved in NK cell expansion and
RT regulation of lymphocyte function.";
RL Nature 408:57-63(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC STRAIN=BALB/c;
RA Guobing C., Jun D., Junsong C., Fenshu Z.;
RT "Mouse Interleukin 21 can improve the anti-tumor effect of LAK
RT cells.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION AND SUBCELLULAR LOCATION.
RX PubMed=11970879; DOI=10.1016/S1074-7613(02)00295-9;
RA Kasaban M.T., Whiters M.J., Carter L.L., Lowe L.D., Juself J.M.,
RA Deng B., Johnson K.A., Mitek J.S., Senices M., Konz R.F.,
RA Wurster A.L., Donaldson D.D., Collins M., Young D.A., Grusby M.J.;
RT "IL-21 limits NK cell responses and promotes antigen-specific T cell
RT activation: a mediator of the transition from innate to adaptive
RT immunity.";
RL Immunity 16:559-569(2002).
RN [4]
RP FUNCTION.
RX PubMed=12893770; DOI=10.1182/blood-2003-03-0669;
RA Brandt K., Bullone-Paus S., Foster D.C., Rueckert R.;
RT "Interleukin-21 inhibits dendritic cell activation and maturation.";
RL Blood 102:4090-4098(2003).
RN [5]
RP FUNCTION.
RX PubMed=15100251;
RA Pene J., Gauduchat J.F., Lecart S., Drouet E., Guglielmi P., Boulay V.,
RA Delwail A., Foster D., Lecron J.C., Yssel H.;
RT "IL-21 is a switch factor for the production of IgG1 and IgG3 by human
RT B cells.";
RL J. Immunol. 172:5154-5157(2004).
CC -!- FUNCTION: Cytokine with immunoregulatory activity. May promote the
CC transition between innate and adaptive immunity. Induces the
CC production of IgG(1) and IgG(3) in B-cells. May play a role in
CC proliferation and maturation of natural killer (NK) cells in
CC synergy with IL15. May regulate proliferation of mature B- and T-
CC cells in response to activating stimuli. In synergy with IL15 and
CC IL18 stimulates interferon gamma production in T-cells and NK
CC cells (By similarity). During T-cell mediated immune response may
CC inhibit dendritic cells (DC) activation and maturation.
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the IL-21 family.
CC -----
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CC -----
DR EMBL: AF254070; AAC29349.1; -; mRNA.
DR EMBL: AY428162; AAR06254.1; -; mRNA.
DR Ensembl: ENSMUSG0000027718; Mus musculus.
DR MGI: MGI:1890474; Il21.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IDA.
DR GO: GO:0045579; P:positive regulation of B cell differentiation; NAS.
DR GO: GO:0001783; P:programmed cell death, B cells; NAS.
KM Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 146 Interleukin-21.
FT FTid=PRO_0000015506.
FT CARBOHYD 85 85 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 64 115 Potential.
FT FT 71 118 Potential.
SQ SEQUENCE 146 AA; 16811 MW; D2527ED95BA15194 CRC64;
Query Match 57.2%; Score 486; DB 1; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.5e-35;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERVICLAWYFLGTLVHKSSSGODRHMIRBQLIDIVDLKXVYNDLVPEFLPAPEDV 67
DB 1 MERVLCVLVIFLGTVAHKSSPGQPDRLIRLRLHLDIVQKLYENDLPELLSAPQDV 60
QY 68 ETNCWMSAFSCFOKAQLKSANTGNERRIINVSIKLKRKPPSTNAGRORHLTCPSGDS 127
DB 61 KGHCEHAAPAFQKAKLKPSPGNKTFILDLVAQLRRRLPARRGKQKHIAKPCSDS 120
QY 128 YEKKPKPEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKPEFLERLKLQKMIHQHLS 146
RESULT 6
Q5SUE2_MOUSE PRELIMINARY; PRT; 146 AA.
ID Q5SUE2_MOUSE
AC Q5SUE2;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Interleukin 21.
GN Name=Il21; ORFNames=DN-452A22.7-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pandian R.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: AL645982; CA126234.1; -; Genomic DNA.
DR Ensembl: ENSMUSG0000027718; Mus musculus.
SQ SEQUENCE 146 AA; 16811 MW; D2527ED95BA15194 CRC64;
Query Match 57.2%; Score 486; DB 2; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.5e-35;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
QY 8 MERVICLAWYFLGTLVHKSSSGODRHMIRBQLIDIVDLKXVYNDLVPEFLPAPEDV 67
DB 1 MERVLCVLVIFLGTVAHKSSPGQPDRLIRLRLHLDIVQKLYENDLPELLSAPQDV 60
QY 68 ETNCWMSAFSCFOKAQLKSANTGNERRIINVSIKLKRKPPSTNAGRORHLTCPSGDS 127
DB 61 KGHCEHAAPAFQKAKLKPSPGNKTFILDLVAQLRRRLPARRGKQKHIAKPCSDS 120
QY 128 YEKKPKPEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKPEFLERLKLQKMIHQHLS 146
RESULT 7
IL21_PERMA STANDARD; PRT; 123 AA.
ID IL21_PERMA
AC O80XG2;
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Interleukin-21 precursor (IL-21) (Fragment).
GN Name=Il21;
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetidae; Neotominae; Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].

RA Schountz T., Buntiger A., Davenport B., Hegg T.:
 RT "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4
 RT CDNA's."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
 CC transition between innate and adaptive immunity. Induces the
 CC production of IgG(1) and IgG(3) in B-cells. May play a role in
 CC proliferation and maturation of natural killer (NK) cells in
 CC synergy with IL15. May regulate proliferation of mature B- and T-
 CC cells in response to activating stimuli. In synergy with IL15 and
 CC IL18 stimulates interferon gamma production in T-cells and NK
 CC cells (By similarity). During T-cell mediated immune response may
 CC inhibit dendritic cells (DC) activation and maturation (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-21 family.
 CC -----
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 CC -----
 DR EMBL: AY247761; AAP04420.1; -; mRNA.
 KM Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 10 Potential.
 FT CHAIN 11 123 Interleukin-21.
 FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).
 FT DISULFID 56 107 Potential.
 FT DISULFID 63 110 Potential.
 FT NON_TER 1 1
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13945 MW; 8656C8EA95447B34 CRC64;
 Query Match 46.1%; Score 392; DB 1; Length 123;
 Best Local Similarity 60.2%; Pred. No. 5.1e-27;
 Matches 74; Conservative 24; Mismatches 25; Indels 0; Gaps 0;
 QY 16 MVIFLGLVHKSSQGDHRMIRNQLIDIVDQKYNVNDLVPEFLPAPEDEVFNCEWSA 75
 DB 1 VVIFLGLVHKSSQGDHRMIRNQLIDIVDQKYNVNDLVPEFLPAPEDEVFNCEWSA 60
 QY 76 FSCFQKQKLSANTGNRRINIVSIKKLKRKPSPTNGRGRKHLLTQPCSCSYKKPKPE 135
 DB 61 PACFQKQKLSANTGNRRINIVSIKKLKRKPSPTNGRGRKHLLTQPCSCSYKKPKPE 120
 QY 136 FLE 138
 DB 121 FLE 123
 RESULT 8
 Q58IU6 CHICK PRELIMINARY; PRT; 145 AA.
 ID Q58IU6 CHICK
 AC Q58IU6
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Interleukin 21.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Shao J., Dong W., Xiang L.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AY943833; AAK40651.1; -; mRNA.
 SQ SEQUENCE 145 AA; 16637 MW; E70AB6A568CDAABE6 CRC64;

Query Match 20.2%; Score 171.5; DB 2; Length 145;
 Best Local Similarity 31.1%; Pred. No. 2.9e-07;
 Matches 47; Conservative 27; Mismatches 62; Indels 15; Gaps 5;
 QY 8 MERIVICLWVIFLGLVHKSSQGDHRMIRNQLIDIVDQKYNVNDLVPEFLPAPEDEV 67
 DB 1 MERIVICLWVIFLGLVHKSSQGDHRMIRNQLIDIVDQKYNVNDLVPEFLPAPEDEV 56
 QY 68 ETNCEWSAFSCFQKQKLSANTGNRRINIVSIKKLKRKPSPTNAGRGRKHLLTQPC 124
 DB 57 GDGCLTLVAVCFQGIKILQPKNSQVWATPAKTVKILRRPEFLPVSEEH-CESS 108
 QY 125 CDSEYKKPKPEFLERFSLQKMIHQHLSR 155
 DB 109 CSEYERKKPKPEFLERFSLQKMIHQHLSR 139
 RESULT 9
 Q38121 TETNG PRELIMINARY; PRT; 145 AA.
 ID Q38121 TETNG
 AC Q38121
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 22-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Interleukin 21.
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygii; Acanthopterygii; Perciformes; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 NC NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA TISSUE=Head kidney;
 RA Wang H., Shao J., Xiang L., Dong W.;
 RT "Molecular cloning and expression analysis of an IL-21 homolog from
 RT Tetraodon nigroviridis."
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: DQ227693; ABB05043.1; -; mRNA.
 SQ SEQUENCE 145 AA; 16523 MW; F8BE28D1E3717818 CRC64;
 Query Match 14.1%; Score 119.5; DB 2; Length 145;
 Best Local Similarity 25.3%; Pred. No. 0.013;
 Matches 41; Conservative 29; Mismatches 57; Indels 35; Gaps 6;
 QY 8 MERIVICLWVIFLGLVHKSSQGDHRMIRNQLIDIVDQKYNVNDLVPEFLPAPEDEV 66
 DB 1 MKQVFLCLFAVCCMWMLADASSACSEKLEVERRELEGVANNVLQN-RELL-LTTPPKN 56
 QY 67 VERNCEWSAFSCF-----QKQKLSANTGNRRINIVSIKKLKRKPSPTNA 112
 DB 57 IEBCCCLSLARCFRDSIQENIKSTVRLQRLYSLNNSHRAACLNFC-----HSENA 108
 QY 113 GRQKRLTQPCSCSYKKPKPEFLERFSLQKMIHQHLSR 154
 DB 109 -----TQTCNSHQEKVGEFFSRHDSFIQAKSKLRSS 142
 RESULT 10
 IL15 FELCA STANDARD; PRT; 162 AA.
 ID IL15 FELCA
 AC O97687
 DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1999, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Interleukin-15 precursor (IL-15).
 GN Name=IL15;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Flesipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE (MENA).
RC TISSUE=Lymph node;
RA Berger A.B., Dean G.A., Lavoy A.S.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytokine that stimulates the proliferation of T-
CC Lymphocytes. Stimulation by IL-15 requires interaction of IL-15
CC with components of IL-2R, including IL-2R beta and probably IL-2R
CC gamma but not IL-2R alpha (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- SIMILARITY: Belongs to the IL-15 family.
CC -----
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CC -----
DR EMBL; AF108148; AAD05268.1; -; mRNA.
DR InterPro; IPR003443; Interleukin_15.
DR PANTHER; PTHR11323; Interleukin_15; 1.
DR Pfam; PF02372; IL15; 1.
DR Cytokine; Glycoprotein; Signal.
KW SIGNAL
FT PROPEP 30 48
FT CHAIN 49 162
FT FTID=PRO_0000015395.
FT CARBOHYD 104 104
FT CARBOHYD 127 127
FT DISULFID 83 133
FT DISULFID 90 136
SQ SEQUENCE 162 AA; 18412 MW; D8C7CEFF740110DD CRC64;

Query Match 12.5%; Score 106.5; DB 1; Length 162;
Best Local Similarity 26.0%; Pred. No. 0.21;
Matches 38; Conservative 25; Mismatches 58; Indels 25; Gaps 6;

QY 14 CLAWIFGLT---VHKSSGQGDHMTMRQLDIVDQKRYVNDVVEFLPAEDVETN 70
DB 30 CIPVFLISCNAGLPKTEANQD--VISDLKTIKIQSLHIDATLYTE---SDVHPN 82
QY 71 CEMSAFSCF---QKAOLKSANTGNERRIIVNISIKLKRKPPSTNAGRQKRLT---CP 123
DB 83 CKVTAMKCFLELHVLVISLESQETIHQVEVITII-----LANSGLSKRNITTCCK 134
QY 124 SCDSYEKKPKPEFLERKSLQKMIH 149
DB 135 ECCELKEKIKELQSFVHIVQMFIN 160

RESULT 11
Q6FGX7 HUMAN PRELIMINARY; PRT; 135 AA.
AC Q6FGX7;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE IL15 protein (Interleukin 15, isoform 2).
GN Name=IL15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schatten R., Shen B., Hense S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=PCR/rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow R.H., Schaefer C.F., Bhut N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toohyuk S., Abramson R.D., Mullaly S.J.,
RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallue D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RC NIH MGC Project;
RG Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
RL [4]
RN NUCLEOTIDE SEQUENCE.
RP Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RA Li C.;
CC -----
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CC -----
DR EMBL; BC100962; AA100963.1; -; mRNA.
DR EMBL; CR542007; CA646804.1; -; mRNA.
DR EMBL; AY720442; AAU21241.1; -; mRNA.
DR EMBL; CR541980; CA646777.1; -; mRNA.
DR EMBL; BC100961; AA100962.1; -; mRNA.
DR Ensembl; ENSG00000164136; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005126; F:hematopoietic/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003443; Interleukin_15.
DR PANTHER; PTHR11323; Interleukin_15; 1.
DR Pfam; PF02372; IL15; 1.
SQ SEQUENCE 135 AA; 14912 MW; EB44P422096B143E CRC64;

Query Match 11.7%; Score 99.5; DB 2; Length 135;
Best Local Similarity 25.9%; Pred. No. 0.72;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

QY 43 IDIVDQKNYVNDLVPEF---LPAPEDVETNCMSAFSCF---QKAOLKSANTGNNE 93
DB 24 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLESQDASIH 82
QY 94 RIIVNSIKLKRKPPSTNAGRQKRLTSCDSYEKKPKPEFLERKSLQKMIH 149
DB 83 TVENLII--LANSLSISNGVNTES--GCKECELKEKIKELQSFVHIVQMFIN 133

RESULT 12
IL15 HUMAN STANDARD; PRT; 162 AA.
ID IL15 HUMAN
AC P40933; O00440; O43512; Q93058; Q9UBA3;
DT 01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1995, sequence version 1.
DT 07-FEB-2006, entry version 43.
DE Interleukin-15 precursor (IL-15).
GN Name=IL15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea
 CC Homo.
 RN NCBI_TaxID=9606.
 RX [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM IL15-S48AA).
 RC TISSUE=Bone marrow;
 RX MEDLINE=94233380; PubMed=817815;
 RA Grabstein K.H., Eisenman J., Shanebeck K., Rauch C., Srinivasan S.,
 Rung V., Beets C., Richardson J., Schoenborn M.A., Andien M.,
 Johnson L., Alderson M.R., Watson J.D., Boernern D.M., Giri J.G.;
 RT "Cloning of a T cell growth factor that interacts with the beta chain
 of the interleukin-2 receptor."
 RL Science 264:965-968(1994).
 RP NUCLEOTIDE SEQUENCE (ISOFORM IL15-S48AA).
 RA Krause H., Jandritz B., Wernicke C., Bulfone-Paue S., Pohl T.,
 Diamantstein T.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM IL15-S21AA).
 RC TISSUE=Lung cancer;
 RX MEDLINE=96218669; PubMed=8666345;
 RA Meazza R., Verdiani S., Biasoni R., Coppolecchia M., Gaggero A.,
 Orenzo A.M., Colombo M.P., Azzone B., Ferrini S.;
 RT "Identification of a novel interleukin-15 (IL-15) transcript isoform
 generated by alternative splicing in human small cell lung cancer cell
 lines."
 RL Oncogene 12:2187-2192(1996).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM IL15-S21AA).
 RC TISSUE=Testis;
 RX MEDLINE=98070771; PubMed=9405633; DOI=10.1073/pnas.94.26.14444;
 RA Tagaya Y., Kury G., Thies T.A., Losi J.M., Azimi N., Hanover J.A.,
 Bamford R.N., Waldman T.A.;
 RT "Generation of secretable and nonsecretable interleukin 15 isoforms
 through alternate usage of signal peptides."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:14444-14449(1997).
 RN [5]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 3).
 RA Meazza R., Ferrini S.;
 RT "Expression of two IL-15 mRNA isoforms in human tumors does not
 correlate with secretion: role of different signal peptides."
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM IL15-S48AA).
 RC TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=14277932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altshul S.F., Zeeberg B., Boone T., Mak S.I., Wang J., Hsieh F.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diachenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 Rana S.S., McQuillan N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 Bonak S.A., Leowanaporn J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
 Villalón D.K., Mozley D.M., Sodegren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Keteeman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Buterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP NUCLEOTIDE SEQUENCE OF 49-162.
 RC TISSUE=Epidermis;
 RA Sorel M.A., Jacques Y.;
 RT "IL15 expression in human keratinocytes".
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.

```
CC CC -1- FUNCTION: Cytokine that stimulates the proliferation of T-lymphocytes. Stimulation by IL-15 requires interaction of IL-15 with components of IL-2R, including IL-2R beta and probably IL-2R gamma but not IL-2R alpha.
```

```
CC CC -1- SUBCELLULAR LOCATION: Secreted (IL15-S48AA). IL15-S21AA is not secreted, but rather is stored intracellularly, appearing in the nucleus and cytoplasmic components.
```

```
CC CC -1- ALTERNATIVE PRODUCTS:
```

```
CC CC Event=Alternative splicing; Named isoforms=3;
```

```
CC CC Name=IL15-S48AA;
```

```
CC CC IsoId=P40933-1; Sequence=Displayed;
```

```
CC CC Name=IL15-S21AA;
```

```
CC CC IsoId=P40933-2; Sequence=VSP_002660;
```

```
CC CC Name=3;
```

```
CC CC IsoId=P40933-3; Sequence=VSP_002661;
```

```
CC CC -1- TISSUE SPECIFICITY: Most abundant in placenta and skeletal muscle. It is also detected in the heart, lung, liver and kidney. IL15-S21AA is preferentially expressed in tissues such as testis and thymus.
```

```
CC CC -1- SIMILARITY: Belongs to the IL-15 family.
```

```
CC CC -1- DATABASE: NCBI System's Cytokine source book: IL15;
```

```
CC CC WWW="http://www.rndsystems.com/asip/g_steblidex.asp?bodyId=209".
```

```
CC CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
```

```
-----
```

```
DR EMBL U14407; AAA21551.1; -, mRNA.
```

```
DR EMBL X91233; CAAG6216.1; -, Genomic DNA.
```

```
DR EMBL X94223; CAAG3914.1; -, mRNA.
```

```
DR EMBL X94222; CAAG3913.1; -, mRNA.
```

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DR EMBL AF031167; AAB97518.1; -, mRNA.
```

```
DR EMBL Y09908; CAA71044.1; -, mRNA.
```

```
DR EMBL BC018149; AAH18149.1; -, mRNA.
```

```
DR EMBL Z38000; CAAB6100.1; -, mRNA.
```

```
DR Ensembl ENSG00000164136; Homo sapiens.
```

```
DR HGNC HGNC:5977; IL15.
```

```
DR MIM 600554; gene.
```

```
DR GO GO:0005768; C:endosome; TAS.
```

```
DR GO GO:0005615; C:extracellular space; TAS.
```

```
DR GO GO:0005794; C:Golgi apparatus; TAS.
```

```
DR GO GO:0005887; C:integral to plasma membrane; TAS.
```

```
DR GO GO:0005624; C:membrane fraction; TAS.
```

```
DR GO GO:0004871; F:signal transducer activity; TAS.
```

```
DR GO GO:0007267; P:cell-cell signaling; TAS.
```

```
DR GO GO:0006955; P:immune response; TAS.
```

```
DR GO GO:0008284; P:positive regulation of cell proliferation; TAS.
```

```
DR GO GO:0007165; P:signal transduction; TAS.
```

```
DR InterPro IPR003443; Interleukin_15.
```

```
DR Pfam PF081123; Interleukin_15; 1.
```

```
DR SMART SMTSLN123; Interleukin_15; 1.
```

```
DR KEGG pf02372; IL15; 1.
```

```
KW Alternative splicing; Cytokine; Glycoprotein; Signal.
```

```
FT SIGNAL 1 29 Potential.
```

```
FT PROPEP 30 48 Potential.
```

```
FT CHAIN 49 162 /FtId=PRO_0000015393.
```

```
FT FT CARBOHYD 127 127 /FtId=PRO_0000015394.
```

```
FT FT DISULFD 83 133 N-linked (GlcNAc...) (Potential).
```

```
FT FT DISULFD 90 136 Potential.
```

```
FT FT VASAPPLIC 1 47 MRKPKHRHSISIQCYCLLNSHRTLAGIHVFILGCFSA
```

```
FT FT GLPTE -> MDFOYQTSFILLSASVMSR (in isoform 3).
```

```
FT FT VASAPPLIC 1 37 /FtId=VSP_002661.
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```
FT FT CONFLICT 141 141 MRKPKHRHSISIQCYCLLNSHFLTAGIHVFILG ->
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```
FT FT SEQUENCE 162 AA; 18086 MW; 0CE0520C1D8379E2 CRC64; /FtId=VSP_002660.
```

```
SO Query March 11.7%; Score 99.5; DB 1; Length 162;
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```
Best Local Similarity 25.9%; Pred.No.0.88;
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```
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5
```

```

Qy 43 IDIVDOLKQNVNDLVPF-----LPAPEDVETNCWMSAFSCF-----OKAOLKSANTGNNE 93
Db 51 VNIISDJKK-IEDIISGMHIDATITYESDVHPSCKVTNMRKFFLELLOVISLESQDASHD 109
Qy 94 RIINVSIIKKRKRPSTNAGRGHRLTSPSCDSYEKKPKPEFLERFKSLLOKMIH 149
Db 110 TVERLII--LANNLSNGNVTES---GCKECELLEKNIKEFLQSFVHIQWFMIN 160

RESULT 13
Q49528_HUMAN
ID Q49528_HUMAN PRELIMINARY; PRT; 162 AA.
AC Q49528;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DE Interleukin 15, isoform 1.
GN Name=IL15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uebin F.B., Toshitoki S., Garinai P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Vallian D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (Aug-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BCJ00963; AA100964.1; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO: GO:0006935; P:immune response; IEA.
SQ SEQUENCE 162 AA; 18086 MW; 0CE0520CID8379E2 CRC64;

Query Match 11.7%; Score 99.5; DB 2; Length 162;
Best Local Similarity 23.9%; Pred. No. 0.88; Indels 15; Gaps 5;
Matches 30; Conservative 23; Mismatches 48;

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RESULT 14
ID Q59902_FUGRU PRELIMINARY; PRT; 155 AA.
AC Q59902;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DE Interleukin-21.
GN Name=IL-21;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Taki fugu.
NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15592926; DOI=10.1007/s00251-004-0741-7;
RA Bird S., Zou J., Kono T., Sakai M., Martins Dijkstra J., Secombe C.;
RT "Characterization and expression analysis of interleukin 2 (IL-2) and
RT IL-21 homologues in the Japanese pufferfish, Fugu rubripes, following
RT the rediscovery by synteny."
RL Immunogenetics 56:909-923(2005).
CC -----
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CC -----
DR EMBL: AJ844554; CAH59638.1; mRNA.
DR EMBL: AJ584837; CAE50922.2; Genomic DNA.
SQ SEQUENCE 155 AA; 17777 MW; 61DEFE96BD52945E CRC64;

Query Match 11.6%; Score 98.5; DB 2; Length 155;
Best Local Similarity 23.6%; Pred. No. 1;
Matches 37; Conservative 33; Mismatches 64; Indels 23; Gaps 6;

Qy 8 MERIVLCIWIYIFGLTVHKSSSGODRHMIRMLQIDIVDOL--KNYVNDLVPFLLPAP 64
Db 1 MKPVLVLCIFAVCCMCVNDASVDK-VQQRKLELIELRLGMVKKRLQNSKMLSTPS 59
Qy 65 EDVETNCWMSAFSCFOKAOLKSANTGNNERIINVS--IKLKRKPSTNAGRR---QK 117
Db 60 ENIGDCCLSLALCKFRE-----NFKEIFSLTDPQKLYRSLTNTLTKEGLDPCDS 110
Qy 118 HRLTSCDSYEKKPKPEFLERFKSLLOKMIHQHLS 154
Db 111 KNSTCODCHSHPEKAKKFFDRNLNSLQKV--HLKS 144

RESULT 15
ID IL15_RABIT STANDARD; PRT; 162 AA.
AC Q35768;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 27-SEP-2005, sequence version 1.
DT 07-MAR-2006, entry version 6.
DE Interleukin-15 precursor (IL-15).
GN Name=IL15;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA], AND TISSUE SPECIFICITY.
RX PubMed=1597671; DOI=10.1016/j.yetimm.2005.04.013;
RA Xiong C., Hixson P.M., Mendoza L.H., Smith C.W.;
RT "Cloning and expression of rabbit interleukin-15."
RL Vet. Immunol. Immunopathol. 107:131-141(2005).
CC -1- FUNCTION: Cytokine that stimulates the proliferation of T-
CC lymphocytes. Stimulation by IL-15 requires interaction of IL-15
CC with components of IL-2R, including IL-2R beta and probably IL-2R

```

CC gamma but not IL-2R alpha (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- TISSUE SPECIFICITY: Expressed in many tissues including heart,
 CC spleen, lung, liver, muscle and kidney (at mRNA level). Expressed
 CC in many tissues including heart, spleen, lung, liver, muscle and
 CC kidney (at protein level).
 CC -1- SIMILARITY: Belongs to the IL-15 family.
 CC -----
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 CC -----
 CC EMBL: DO157452; AA282803.1; -. mRNA.
 CC InterPro: IPR003443; Interleukin_15.
 CC PANTHER: PTHR11323; Interleukin_15; 1.
 CC Pfam: PF02372; IL15; 1.
 CC KMW Cytokine; Glycoprotein; Signal.
 CC FT SIGNAL 1 29 Potential.
 CC PROPER 30 48 Potential.
 CC FT CHAIN 49 162 /FTid=PRO_0000043393.
 CC FT CARBOHYD 108 108 /FTid=PRO_0000043394.
 CC FT CARBOHYD 119 119 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).
 CC FT DISULFID 83 133 Potential.
 CC FT DISULFID 90 136 Potential.
 CC SQ SEQUENCE 162 AA; 18330 MW; 6F9C7CC129FB64B9 CRC64;

Query Match 11.6%; Score 98.5; DB 1; Length 162;
 Best Local Similarity 27.1%; Pred. No. 1.1;
 Matches 32; Conservative 17; Mismatches 48; Indels 21; Gaps 5;

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 Db 52 DVISDLKR-IEDLKSIHIDATLYTESDAHNCVTAMKCFLELRVISHESRMNDINET 110
 Qy 95 IINVSIT--KKLKKRPSTNAGRQKRLTCTPCSDSYEKKPKPELLEFKSLQKMIH 149
 Db 111 VQNLIIANTSLSSKGNVTESG-----CKECELEEKNTIEFLQSFHIVQMFIN 160

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 Job time : 91.3314 secs

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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:51:46; Search time 16.2 Seconds
(without alignments)
875.306 Million cell updates/sec

Title: US-10-659-684-2

Perfect score: 850
Sequence: 1 MRSSPGNNRIVICLMTVFL.....LLQKMIHQHLSRTHGSEDS 162

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB pep: *
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB pep: *
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB pep: *
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB pep: *
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCYUS_COMB pep: *
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB pep: *
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfilltest pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850	100.0	162	2	US-09-522-217-2 Sequence 2, Appli
2	850	100.0	162	2	US-09-923-246-2 Sequence 2, Appli
3	850	100.0	162	2	US-10-295-723-2 Sequence 2, Appli
4	850	100.0	162	2	US-09-825-561A-10 Sequence 10, Appli
5	850	100.0	162	2	US-10-282-622-2 Sequence 2, Appli
6	850	100.0	174	2	US-09-949-016-10307 Sequence 10307, A
7	831	97.8	162	2	US-10-282-622-6 Sequence 4, Appli
8	758	89.2	147	2	US-10-282-622-4 Sequence 85, Appli
9	695.5	81.8	519	2	US-09-522-217-85 Sequence 85, Appli
10	695.5	81.8	519	2	US-09-923-246-85 Sequence 85, Appli
11	695.5	81.8	519	2	US-10-295-723-85 Sequence 85, Appli
12	486	57.2	146	2	US-09-522-217-56 Sequence 56, Appli
13	486	57.2	146	2	US-09-923-246-56 Sequence 56, Appli
14	486	57.2	146	2	US-10-295-723-56 Sequence 56, Appli
15	486	57.2	146	2	US-09-825-561A-47 Sequence 47, Appli
16	394	46.4	510	2	US-09-522-217-89 Sequence 89, Appli
17	394	46.4	510	2	US-09-923-246-89 Sequence 89, Appli
18	394	46.4	510	2	US-10-295-723-89 Sequence 89, Appli
19	212	24.9	40	2	US-09-522-217-72 Sequence 72, Appli
20	212	24.9	40	2	US-09-923-246-72 Sequence 72, Appli
21	212	24.9	40	2	US-10-295-723-72 Sequence 72, Appli
22	176	20.7	32	2	US-09-522-217-73 Sequence 73, Appli
23	176	20.7	32	2	US-09-923-246-73 Sequence 73, Appli
24	176	20.7	32	2	US-10-295-723-73 Sequence 73, Appli
25	99.5	11.7	114	1	US-08-031-399-6 Sequence 6, Appli
26	99.5	11.7	114	1	US-08-031-399-12 Sequence 12, Appli

27	99.5	11.7	114	1	US-08-393-305-3 Sequence 3, Appli
28	99.5	11.7	114	1	US-08-726-817-3 Sequence 3, Appli
29	99.5	11.7	114	1	US-08-504-042-6 Sequence 6, Appli
30	99.5	11.7	114	1	US-08-504-042-12 Sequence 12, Appli
31	99.5	11.7	114	1	US-08-725-969-3 Sequence 3, Appli
32	99.5	11.7	114	1	US-08-794-524-3 Sequence 3, Appli
33	99.5	11.7	114	2	US-09-189-193-3 Sequence 3, Appli
34	99.5	11.7	114	2	US-09-462-941-20 Sequence 20, Appli
35	99.5	11.7	114	5	PCT-US94-03793-6 Sequence 6, Appli
36	99.5	11.7	114	5	PCT-US94-03793-12 Sequence 12, Appli
37	99.5	11.7	162	1	US-08-031-399-5 Sequence 5, Appli
38	99.5	11.7	162	1	US-08-393-305-2 Sequence 2, Appli
39	99.5	11.7	162	1	US-08-535-733-2 Sequence 2, Appli
40	99.5	11.7	162	1	US-08-726-817-2 Sequence 2, Appli
41	99.5	11.7	162	1	US-08-504-042-5 Sequence 5, Appli
42	99.5	11.7	162	1	US-08-725-969-2 Sequence 2, Appli
43	99.5	11.7	162	1	US-08-794-524-2 Sequence 2, Appli
44	99.5	11.7	162	2	US-08-842-947-6 Sequence 6, Appli
45	99.5	11.7	162	2	US-09-189-193-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-522-217-2
; Sequence 2, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Preenell, Cindy R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Grose, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-2

Query Match 100.0%; Score 850; DB 2; Length 162;

Best Local Similarity 100.0%; Pred. No. 1.4e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRSSPGNNRIVICLMTVFLCTLVHKSSQCDRHMTMRQLIDIVDOLKRYVNDLVEF	60
DB	1	MRSSPGNNRIVICLMTVFLCTLVHKSSQCDRHMTMRQLIDIVDOLKRYVNDLVEF	60
QY	61	LPAPEDVTNEMWAFSCFOKAOLKSANTGNERRIINVSICKLKRKPPSTNAGRORGRRL	120
DB	61	LPAPEDVTNEMWAFSCFOKAOLKSANTGNERRIINVSICKLKRKPPSTNAGRORGRRL	120
QY	121	TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS	162
DB	121	TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS	162

```
RESULT 2
US-09-923-246-2
; Sequence 2, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-2

Query Match      100.0%; Score 850; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,4e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRSSPGNMERIVICLWYIFLGTLVHKSSSGODRHMIRMQLDIDVDQLKNYVNDLVPEF 60
DB      1 MRSSPGNMERIVICLWYIFLGTLVHKSSSGODRHMIRMQLDIDVDQLKNYVNDLVPEF 60
QY      61 LPAPEDVETNCESAFSCFQKQOLKSANTGNMERIINVSIKLKRKPPSTNAGRQGRRL 120
DB      61 LPAPEDVETNCESAFSCFQKQOLKSANTGNMERIINVSIKLKRKPPSTNAGRQGRRL 120
QY      121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB      121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 3
US-10-295-723-2
; Sequence 2, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
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; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-2

Query Match      100.0%; Score 850; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,4e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRSSPGNMERIVICLWYIFLGTLVHKSSSGODRHMIRMQLDIDVDQLKNYVNDLVPEF 60
DB      1 MRSSPGNMERIVICLWYIFLGTLVHKSSSGODRHMIRMQLDIDVDQLKNYVNDLVPEF 60
QY      61 LPAPEDVETNCESAFSCFQKQOLKSANTGNMERIINVSIKLKRKPPSTNAGRQGRRL 120
DB      61 LPAPEDVETNCESAFSCFQKQOLKSANTGNMERIINVSIKLKRKPPSTNAGRQGRRL 120
QY      121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB      121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 4
US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-10

Query Match      100.0%; Score 850; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,4e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRSSPGNMERIVICLWYIFLGTLVHKSSSGODRHMIRMQLDIDVDQLKNYVNDLVPEF 60
DB      1 MRSSPGNMERIVICLWYIFLGTLVHKSSSGODRHMIRMQLDIDVDQLKNYVNDLVPEF 60
QY      61 LPAPEDVETNCESAFSCFQKQOLKSANTGNMERIINVSIKLKRKPPSTNAGRQGRRL 120
DB      61 LPAPEDVETNCESAFSCFQKQOLKSANTGNMERIINVSIKLKRKPPSTNAGRQGRRL 120
QY      121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB      121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
```

RESULT 5
US-10-282-622-2
Sequence 2, Application US/10282622
Patent No. 6929932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 6929932ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-282-622-2

Query Match 100.0%; Score 850; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.4e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRSSPGNNRIVICLVIFLGLTVHKSSOGODRHIMRROLIDIVDOLKNYVNDLVEEF 60
Db 1 MRSSPGNNRIVICLVIFLGLTVHKSSOGODRHIMRROLIDIVDOLKNYVNDLVEEF 60
Oy 61 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIVSIKLRKPPSTNAGRORQKRL 120
Db 61 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIVSIKLRKPPSTNAGRORQKRL 120
Oy 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 6
US-09-949-016-10307
Sequence 10307, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10307
LENGTH: 174
TYPE: PRT
ORGANISM: Human
US-09-949-016-10307

Query Match 100.0%; Score 850; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.5e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRSSPGNNRIVICLVIFLGLTVHKSSOGODRHIMRROLIDIVDOLKNYVNDLVEEF 60
Db 13 MRSSPGNNRIVICLVIFLGLTVHKSSOGODRHIMRROLIDIVDOLKNYVNDLVEEF 72

Oy 61 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIVSIKLRKPPSTNAGRORQKRL 120
Db 73 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIVSIKLRKPPSTNAGRORQKRL 132
Oy 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db 133 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 174

RESULT 7
US-10-282-622-6
Sequence 6, Application US/10282622
Patent No. 6929932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 6929932ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 162
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: zalp111 ligand Q153D/I156D
US-10-282-622-6

Query Match 97.8%; Score 831; DB 2; Length 162;
Best Local Similarity 98.1%; Pred. No. 1.8e-84;
Matches 159; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MRSSPGNNRIVICLVIFLGLTVHKSSOGODRHIMRROLIDIVDOLKNYVNDLVEEF 60
Db 1 MRSSPGNNRIVICLVIFLGLTVHKSSOGODRHIMRROLIDIVDOLKNYVNDLVEEF 60
Oy 61 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIVSIKLRKPPSTNAGRORQKRL 120
Db 61 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIVSIKLRKPPSTNAGRORQKRL 120
Oy 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 8
US-10-282-622-4
Sequence 4, Application US/10282622
Patent No. 6929932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 6929932ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 147
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: zalp111 ligand Q153ST/I156D
US-10-282-622-4

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Query Match      89.2%; Score 758; DB 2; Length 147;
Best Local Similarity 98.6%; Pred. No. 2.1e-76;
Matches 145; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRSSPGNNRIVICLWVIFLGLTVHKSSSGQODRHIMRQLIDIVDLKKNVNDLVPEF 60
    |||
Db 1 MDSSPGNNRIVICLWVIFLGLTVHKSSSGQODRHIMRQLIDIVDLKKNVNDLVPEF 60

Qy 61 LPAPDEVETNCWSAFSCFQAOLKSANTGNNRINIVSIKKLRKPPSTNAGRQKRL 120
    |||
Db 61 LPAPDEVETNCWSAFSCFQAOLKSANTGNNRINIVSIKKLRKPPSTNAGRQKRL 120

Qy 121 TCPSCDSEYKKPKPEFLERFKSLQKM 147
    |||
Db 121 TCPSCDSEYKKPKPEFLERFKSLQKM 147

RESULT 9
US-09-522-217-85
; Sequence 85, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalpha11 ligand fusion polypeptide
US-09-522-217-85

Query Match      81.8%; Score 695.5; DB 2; Length 519;
Best Local Similarity 95.7%; Pred. No. 9.6e-69;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 23 LVHSSSGQODRHIMRQLIDIVDLKKNVNDLVPEFLPAPDEVETNCWSAFSCFOKA 82
    |||
Db 383 LVPRGS---QDRHMIRKQLIDIVDLKKNVNDLVPEFLPAPDEVETNCWSAFSCFOKA 439

Qy 83 QLSKSGNNRINIVSIKKLRKPPSTNAGRQKRLTSCDSYKKPKPEFLERFKS 142
    |||
Db 440 QLSKSGNNRINIVSIKKLRKPPSTNAGRQKRLTSCDSYKKPKPEFLERFKS 499

Qy 143 LLOQMIIHQLSSRTHGSEDS 162
    |||
Db 500 LLOQMIIHQLSSRTHGSEDS 519

RESULT 10
US-09-923-246-85
; Sequence 85, Application US/09923246
```

```
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalpha11 ligand fusion polypeptide
US-09-923-246-85

Query Match      81.8%; Score 695.5; DB 2; Length 519;
Best Local Similarity 95.7%; Pred. No. 9.6e-69;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 23 LVHSSSGQODRHIMRQLIDIVDLKKNVNDLVPEFLPAPDEVETNCWSAFSCFOKA 82
    |||
Db 383 LVPRGS---QDRHMIRKQLIDIVDLKKNVNDLVPEFLPAPDEVETNCWSAFSCFOKA 439

Qy 83 QLSKSGNNRINIVSIKKLRKPPSTNAGRQKRLTSCDSYKKPKPEFLERFKS 142
    |||
Db 440 QLSKSGNNRINIVSIKKLRKPPSTNAGRQKRLTSCDSYKKPKPEFLERFKS 499

Qy 143 LLOQMIIHQLSSRTHGSEDS 162
    |||
Db 500 LLOQMIIHQLSSRTHGSEDS 519

RESULT 11
US-10-295-723-85
; Sequence 85, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
```

PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: US 60/142,013
 PRIOR FILING DATE: 1999-07-01
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 85
 LENGTH: 519
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: MBP-human zalphal1 ligand fusion polypeptide
 US-10-295-723-85

Query Match 81.8%; Score 695.5; DB 2; Length 519;
 Best Local Similarity 95.7%; Pred. No. 9.6e-69;
 Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 23 LVHSSSGODRHMRQLIDIVDLKYNVNDLVPEFLPAPEVETNCESAFSCFOKA 82
 DB 383 LVPRGS--QDRHMRQLIDIVDLKYNVNDLVPEFLPAPEVETNCESAFSCFOKA 439
 QY 83 QLSANTGNNRRIINVSIKLKRKPPSTNAGRQKRLTSPSCSYEKKEPKEFLERFKS 142
 DB 440 QLSANTGNNRRIINVSIKLKRKPPSTNAGRQKRLTSPSCSYEKKEPKEFLERFKS 499
 QY 143 LLOKMIHQHLSRTHSEDS 162
 DB 500 LLOKMIHQHLSRTHSEDS 519

RESULT 12
 US-09-522-217-56
 Sequence 56, Application US/09522217
 Patent No. 6307024
 GENERAL INFORMATION:
 APPLICANT: No. 6307024ak, Julia E.
 APPLICANT: Premeil, Scott R.
 APPLICANT: Sprecher, Cindy A.
 APPLICANT: Foster, Donald C.
 APPLICANT: Holly, Richard D.
 APPLICANT: Gross, Jane A.
 APPLICANT: Johnston, Janet V.
 APPLICANT: Nelson, Andrew J.
 APPLICANT: Dillon, Stacey R.
 APPLICANT: Hammond, Angela K.
 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
 FILE REFERENCE: 99-16
 CURRENT APPLICATION NUMBER: US/09/522,217
 CURRENT FILING DATE: 2000-03-09
 EARLIER APPLICATION NUMBER: US 60/123,547
 EARLIER FILING DATE: 1999-03-09
 EARLIER APPLICATION NUMBER: US 60/123,904
 EARLIER FILING DATE: 1999-03-11
 EARLIER APPLICATION NUMBER: US 60/142,013
 EARLIER FILING DATE: 1999-07-01
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 56
 LENGTH: 146
 TYPE: PRT
 ORGANISM: mus musculus
 US-09-522-217-56

Query Match 57.2%; Score 486; DB 2; Length 146;
 Best Local Similarity 63.0%; Pred. No. 3.7e-46;
 Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
 QY 8 MERIVICLWVIFGLTVHSSSGODRHMRQLIDIVDLKYNVNDLVPEFLPAPEV 67
 DB 1 MERTLVCLVIVFGLTVHSSSGODRHMRQLIDIVDLKYNVNDLVPEFLPAPEV 60
 QY 68 ETNCEMAFSCFOKAQLKSANTGNNRRIINVSIKLKRKPPSTNAGRQKRLTSPSCDS 127

DB 61 KGHCEHAFAFCFOKAKLKPSNPNNKTFILDLVAQLRRRLPARRGCKQKHIAKCPSCDS 120
 QY 128 YEKKPKPEFLERFKSLLOKMIHQHLS 153
 DB 121 YEKRTPEFLERLKLMLLOKMIHQHLS 146

RESULT 13
 US-09-923-246-56
 Sequence 56, Application US/09923246
 Patent No. 6605272
 GENERAL INFORMATION:
 APPLICANT: No. 6605272ak, Julia E.
 APPLICANT: Premeil, Scott R.
 APPLICANT: Sprecher, Cindy A.
 APPLICANT: Foster, Donald C.
 APPLICANT: Holly, Richard D.
 APPLICANT: Gross, Jane A.
 APPLICANT: Johnston, Janet V.
 APPLICANT: Nelson, Andrew J.
 APPLICANT: Dillon, Stacey R.
 APPLICANT: Hammond, Angela K.
 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
 FILE REFERENCE: 99-16
 CURRENT APPLICATION NUMBER: US/09/923,246
 CURRENT FILING DATE: 2001-08-03
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
 PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 56
 LENGTH: 146
 TYPE: PRT
 ORGANISM: mus musculus
 US-09-923-246-56

Query Match 57.2%; Score 486; DB 2; Length 146;
 Best Local Similarity 63.0%; Pred. No. 3.7e-46;
 Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
 QY 8 MERIVICLWVIFGLTVHSSSGODRHMRQLIDIVDLKYNVNDLVPEFLPAPEV 67
 DB 1 MERTLVCLVIVFGLTVHSSSGODRHMRQLIDIVDLKYNVNDLVPEFLPAPEV 60
 QY 68 ETNCEMAFSCFOKAQLKSANTGNNRRIINVSIKLKRKPPSTNAGRQKRLTSPSCDS 127
 DB 61 KGHCEHAFAFCFOKAKLKPSNPNNKTFILDLVAQLRRRLPARRGCKQKHIAKCPSCDS 120
 QY 128 YEKKPKPEFLERFKSLLOKMIHQHLS 153
 DB 121 YEKRTPEFLERLKLMLLOKMIHQHLS 146

RESULT 14
 US-10-295-723-56
 Sequence 56, Application US/10295723
 Patent No. 6686178
 GENERAL INFORMATION:
 APPLICANT: No. 6686178ak, Julia E.
 APPLICANT: Premeil, Scott R.
 APPLICANT: Sprecher, Cindy A.
 APPLICANT: Foster, Donald C.
 APPLICANT: Holly, Richard D.
 APPLICANT: Gross, Jane A.
 APPLICANT: Johnston, Janet V.
 APPLICANT: Nelson, Andrew J.
 APPLICANT: Dillon, Stacey R.
 APPLICANT: Hammond, Angela K.
 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:52:41 ; Search time 58.7829 Seconds
(without alignments)
1276.576 Million cell updates/sec

Title: US-10-659-684-2

Perfect score: 850

Sequence: 1 MRSSPGNMERIVICLWVIFL.....LLQKMIHQHLSRTHGSEDS 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850	100.0	162	3	US-09-923-246-2
2	850	100.0	162	3	US-09-825-561A-10
3	850	100.0	162	3	US-09-972-218A-19
4	850	100.0	162	4	US-10-264-634-19
5	850	100.0	162	4	US-10-295-723-2
6	850	100.0	162	4	US-10-282-622-2
7	850	100.0	162	4	US-10-456-780-2
8	850	100.0	162	4	US-10-659-684-2
9	850	100.0	162	4	US-10-620-168-2
10	850	100.0	162	5	US-10-872-087-10
11	850	100.0	162	5	US-10-787-442-2
12	850	100.0	162	5	US-10-951-239-2
13	850	100.0	162	5	US-10-775-204-2177
14	850	100.0	162	6	US-11-174-398-2
15	850	100.0	162	6	US-11-134-489-2
16	850	100.0	162	6	US-11-132-947-9
17	850	100.0	162	6	US-11-197-488-19
18	840	98.8	160	6	US-11-197-221-1
19	831	97.8	162	4	US-10-282-622-6
20	831	97.8	162	4	US-11-174-398-6
21	758	89.2	147	6	US-10-282-622-4
22	758	89.2	147	6	US-11-174-398-4
23	708.5	83.4	742	5	US-10-775-204-2167
24	706	83.1	133	3	US-10-867-992-19
25	695.5	81.8	519	5	US-09-923-246-85
26	695.5	81.8	519	4	US-10-295-723-85
27	695.5	81.8	519	4	US-10-659-684-85

28	695.5	81.8	519	5	US-10-787-442-85	Sequence 85, Appl
29	695	81.8	131	5	US-10-867-992-16	Sequence 16, Appl
30	695	81.8	131	6	US-11-132-947-2	Sequence 2, Appl
31	661	77.8	133	5	US-10-867-992-12	Sequence 12, Appl
32	656	77.2	133	5	US-10-867-992-14	Sequence 14, Appl
33	650	76.5	131	5	US-10-867-992-10	Sequence 10, Appl
34	648	76.2	152	6	US-11-132-947-12	Sequence 12, Appl
35	648	75.9	131	5	US-10-867-992-4	Sequence 4, Appl
36	645	75.9	131	5	US-10-867-992-6	Sequence 6, Appl
37	644	75.8	131	5	US-10-867-992-8	Sequence 8, Appl
38	642	75.5	131	5	US-10-867-992-2	Sequence 2, Appl
39	486	57.2	146	3	US-09-923-246-56	Sequence 56, Appl
40	486	57.2	146	3	US-09-825-561A-47	Sequence 47, Appl
41	486	57.2	146	4	US-10-295-723-56	Sequence 56, Appl
42	486	57.2	146	4	US-10-456-780-4	Sequence 4, Appl
43	486	57.2	146	4	US-10-659-684-56	Sequence 56, Appl
44	486	57.2	146	5	US-10-872-087-47	Sequence 47, Appl
45	486	57.2	146	5	US-10-787-442-56	Sequence 56, Appl

ALIGNMENTS

```
RESULT 1
US-09-923-246-2
Sequence 2, Application US/09923246
Patent No. US20020128446A1
GENERAL INFORMATION:
APPLICANT: No. US20020128446A1ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-923-246-2
Query Match 100.0%; Score 850; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSQODRHMRMLIIVDLKRYVNDLVPEF 60
DB 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSQODRHMRMLIIVDLKRYVNDLVPEF 60
QY 61 LPAPEDVTNENWAFSCFOKALOKSANTGNERNIINVSIKKLKRKPPSTNAGRORAKRL 120
DB 61 LPAPEDVTNENWAFSCFOKALOKSANTGNERNIINVSIKKLKRKPPSTNAGRORAKRL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
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RESULT 2
US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-10

Query Match      100.0%; Score 850; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIVDLKYNVNDLVPEF 60
Db      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIVDLKYNVNDLVPEF 60

Qy      61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRQGRHL 120
Db      61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRQGRHL 120

Qy      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 3
US-09-972-218A-19
; Sequence 19, Application US/09972218A
; Publication No. US20030049798A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Laura
; APPLICANT: Whiters, Matthew J
; APPLICANT: Collins, Mary
; APPLICANT: Young, Deborah A.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lowe, Leslie D.
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MO-1, Member of the Cytokine Receptor Family
; FILE REFERENCE: 22058-552CIP2
; CURRENT APPLICATION NUMBER: US/09/972,218A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/569384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/560766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US/6057128
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
US-09-972-218A-19
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Query Match      100.0%; Score 850; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIVDLKYNVNDLVPEF 60
Db      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIVDLKYNVNDLVPEF 60

Qy      61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRQGRHL 120
Db      61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRQGRHL 120

Qy      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 4
US-10-264-634-19
; Sequence 19, Application US/10264634
; Publication No. US20030108549A1
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra et al.
; TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor Ac
; FILE REFERENCE: GI5320-P3
; CURRENT APPLICATION NUMBER: US/10/264,634
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 09/040,005
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 09/560,766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/569,384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/972,218
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/373,746
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
US-10-264-634-19

Query Match      100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIVDLKYNVNDLVPEF 60
Db      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIVDLKYNVNDLVPEF 60

Qy      61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRQGRHL 120
Db      61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRQGRHL 120

Qy      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 5
US-10-295-723-2
; Sequence 2, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
```



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; APPLICANT: Grose, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-723-2

Query Match      100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLAWIFLGTLVHKSSSGODRHMIRMOQLIDIVOLKNYVNDLVPEF 60
DB 1 MRSSPGNMERIVICLAWIFLGTLVHKSSSGODRHMIRMOQLIDIVOLKNYVNDLVPEF 60
QY 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSIIKILKRKPPSTNAGRQGRRL 120
DB 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSIIKILKRKPPSTNAGRQGRRL 120
QY 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 6
US-10-282-622-2
; Sequence 2, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Premeil, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-282-622-2

Query Match      100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLAWIFLGTLVHKSSSGODRHMIRMOQLIDIVOLKNYVNDLVPEF 60
DB 1 MRSSPGNMERIVICLAWIFLGTLVHKSSSGODRHMIRMOQLIDIVOLKNYVNDLVPEF 60
QY 1 MRSSPGNMERIVICLAWIFLGTLVHKSSSGODRHMIRMOQLIDIVOLKNYVNDLVPEF 60
DB 1 MRSSPGNMERIVICLAWIFLGTLVHKSSSGODRHMIRMOQLIDIVOLKNYVNDLVPEF 60
QY 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSIIKILKRKPPSTNAGRQGRRL 120
DB 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSIIKILKRKPPSTNAGRQGRRL 120
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; APPLICANT: Grose, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-723-2

Query Match      100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLAWIFLGTLVHKSSSGODRHMIRMOQLIDIVOLKNYVNDLVPEF 60
DB 1 MRSSPGNMERIVICLAWIFLGTLVHKSSSGODRHMIRMOQLIDIVOLKNYVNDLVPEF 60
QY 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSIIKILKRKPPSTNAGRQGRRL 120
DB 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSIIKILKRKPPSTNAGRQGRRL 120
QY 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 7
US-10-456-780-2
; Sequence 2, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
; TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
; FILE REFERENCE: 03-08
; CURRENT APPLICATION NUMBER: US/10/456,780
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,127
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-456-780-2

Query Match      100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLAWIFLGTLVHKSSSGODRHMIRMOQLIDIVOLKNYVNDLVPEF 60
DB 1 MRSSPGNMERIVICLAWIFLGTLVHKSSSGODRHMIRMOQLIDIVOLKNYVNDLVPEF 60
QY 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSIIKILKRKPPSTNAGRQGRRL 120
DB 61 LPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSIIKILKRKPPSTNAGRQGRRL 120
QY 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 8
US-10-659-684-2
; Sequence 2, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Premeil, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Grose, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRN
ORGANISM: Homo sapiens
US-10-659-684-2

Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGMERIVICLWYIFLGTLVHSSSGQGDHMI RMQLIDIVQLKNYVNDLVEF 60
DB 1 MRSSPGMERIVICLWYIFLGTLVHSSSGQGDHMI RMQLIDIVQLKNYVNDLVEF 60
QY 61 LPADEVETNCESAFSCFOAQLKSANTGNNERIIIVSIKLRKRPSTNAGRORHRL 120
DB 61 LPADEVETNCESAFSCFOAQLKSANTGNNERIIIVSIKLRKRPSTNAGRORHRL 120
QY 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 9
US-10-620-169-2
Sequence 2, Application US/10620169
Publication No. US20040136954A1
GENERAL INFORMATION:
APPLICANT: Grubby, Michael J
APPLICANT: Wurster, Andrea
APPLICANT: Young, Deborah
APPLICANT: Collins, Mary
APPLICANT: Whiters, Matthew
TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
FILE REFERENCE: 22058-585
CURRENT APPLICATION NUMBER: US/10/620,169
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,160
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/403,001
PRIOR FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 162
TYPE: PRN
ORGANISM: Homo sapiens
US-10-620-169-2

Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGMERIVICLWYIFLGTLVHSSSGQGDHMI RMQLIDIVQLKNYVNDLVEF 60
DB 1 MRSSPGMERIVICLWYIFLGTLVHSSSGQGDHMI RMQLIDIVQLKNYVNDLVEF 60
QY 61 LPADEVETNCESAFSCFOAQLKSANTGNNERIIIVSIKLRKRPSTNAGRORHRL 120
DB 61 LPADEVETNCESAFSCFOAQLKSANTGNNERIIIVSIKLRKRPSTNAGRORHRL 120
QY 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 10
US-10-872-087-10

Sequence 10, Application US/10872087
Publication No. US20040235743A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Novak, Julia E.
APPLICANT: West, James W.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA1 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22D1
CURRENT APPLICATION NUMBER: US/10/872,087
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 09/825,561
PRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 162
TYPE: PRN
ORGANISM: Homo sapiens
US-10-872-087-10

Query Match 100.0%; Score 850; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81; Indels 0; Gaps 0;
Matches 162; Conservative 0; Mismatches 0;

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DB 1 MRSSPGMERIVICLWYIFLGTLVHSSSGQGDHMI RMQLIDIVQLKNYVNDLVEF 60
QY 61 LPADEVETNCESAFSCFOAQLKSANTGNNERIIIVSIKLRKRPSTNAGRORHRL 120
DB 61 LPADEVETNCESAFSCFOAQLKSANTGNNERIIIVSIKLRKRPSTNAGRORHRL 120
QY 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 11
US-10-787-442-2
Sequence 2, Application US/10787442
Publication No. US20040260065A1
GENERAL INFORMATION:
APPLICANT: Novak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/787,442
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,504
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2

LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-787-442-2

Query Match
Best Local Similarity 100.0%; Score 850; DB 5; Length 162;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGODRHIMRMQLIDIVDQLKNYVNDLVPER 60
DB 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGODRHIMRMQLIDIVDQLKNYVNDLVPER 60
QY 61 LPAPEDEVETNCESAFSCFOKQOLKSANTGNNEIRIINVSIKKLKRKPPSTNAGRQGRHL 120
DB 61 LPAPEDEVETNCESAFSCFOKQOLKSANTGNNEIRIINVSIKKLKRKPPSTNAGRQGRHL 120
QY 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 12
US-10-951-239-2
Sequence 2, Application US/10951239
Publication No. US2005095223A1
GENERAL INFORMATION:
APPLICANT: Sivakumar, Pallavar
APPLICANT: Nelson, Andrew
TITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES
FILE REFERENCE: 03-09
CURRENT APPLICATION NUMBER: US/10/951,239
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: 60/505,919
PRIOR FILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-951-239-2

Query Match
Best Local Similarity 100.0%; Score 850; DB 5; Length 162;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGODRHIMRMQLIDIVDQLKNYVNDLVPER 60
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QY 61 LPAPEDEVETNCESAFSCFOKQOLKSANTGNNEIRIINVSIKKLKRKPPSTNAGRQGRHL 120
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QY 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 13
US-10-775-204-2177
Sequence 2177, Application US/10775204
Publication No. US2005018666A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Haseltine, William A.
APPLICANT: Balance, David J.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/10/775,204

CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2177
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-775-204-2177

Query Match
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Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LPAPEDEVETNCESAFSCFOKQOLKSANTGNNEIRIINVSIKKLKRKPPSTNAGRQGRHL 120
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QY 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 14
US-11-174-398-2
Sequence 2, Application US/11174398
Publication No. US20050244930A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: Novak, Julia E.
TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/11/174,398
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US/10/282,622
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-11-174-398-2

Query Match
Best Local Similarity 100.0%; Score 850; DB 6; Length 162;
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Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 LPAPEDEVETNCENSAFSCFQQAOLKSANTGNNERIIIVSIIKLRKPPSTNAGRQKRL 120

Db 61 LPAPEDEVETNCENSAFSCFQQAOLKSANTGNNERIIIVSIIKLRKPPSTNAGRQKRL 120

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Db 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 15

US-11-134-489-2

; Sequence 2, Application US/11/134489

; Publication No. US20050265966A1

; GENERAL INFORMATION:

; APPLICANT: Kindsvogel, Wayne R.

; APPLICANT: Hughes, Steven D.

; APPLICANT: Holly, Richard D.

; APPLICANT: Clegg, Christopher H.

; APPLICANT: Foster, Donald C.

; APPLICANT: Johnson, Rebecca A.

; APPLICANT: Heipel, Mark D.

; APPLICANT:Sivakumar, Pallavur V.

; TITLE OF INVENTION: METHODS OF TREATING CANCER USING IL-21 AND MONOCLONAL ANTIBODY TH

; FILE REFERENCE: 04-03

; CURRENT APPLICATION NUMBER: US/11/134,489

; CURRENT FILING DATE: 2005-05-20

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 162

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-134-489-2

Query Match 100.0%; Score 850; DB 6; Length 162;

Best Local Similarity 100.0%; Pred. No. 2e-81;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRSSPGNMERIVICLMTIFLGTLVHKSSSGQDRHMRMROLIDIVDLKYNVNDLVPEF 60

Qy 61 LPAPEDEVETNCENSAFSCFQQAOLKSANTGNNERIIIVSIIKLRKPPSTNAGRQKRL 120

Db 61 LPAPEDEVETNCENSAFSCFQQAOLKSANTGNNERIIIVSIIKLRKPPSTNAGRQKRL 120

Qy 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

Db 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

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Job time : 59.2829 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:53:56 ; Search time 9.95143 Seconds

(without alignments)
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Title: US-10-659-684-2

Perfect score: 850
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Searched: 254368 seqs, 70249769 residues

Total number of hits satisfying chosen parameters: 254368

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	162	US-10-511-937-2572	Sequence 2572, Ap
2	850	100.0	162	US-10-735-149-2	Sequence 2, Appl
3	850	100.0	162	US-10-806-611-10	Sequence 10, Appl
4	850	100.0	162	US-11-429-276-2177	Sequence 2177, Ap
5	708.5	83.4	174	US-11-429-276-2167	Sequence 2167, Ap
6	706	83.1	134	US-10-735-149-28	Sequence 28, Appl
7	695	81.8	131	US-10-806-611-2	Sequence 2, Appl
8	524	61.6	122	US-10-806-611-12	Sequence 12, Appl
9	486	57.2	146	US-10-806-611-13	Sequence 13, Appl
10	394	46.4	122	US-10-806-611-4	Sequence 4, Appl
11	99.5	11.7	162	US-10-511-937-2499	Sequence 2499, Ap
12	82	9.6	605	US-11-429-276-1162	Sequence 1162, Ap
13	76.5	9.0	864	US-11-251-208-77	Sequence 77, Appl
14	74.5	8.8	431	US-11-056-355B-36356	Sequence 36356, A
15	74.5	8.8	431	US-11-056-355B-45283	Sequence 45283, A
16	74.5	8.8	441	US-11-056-355B-36355	Sequence 36355, A
17	74.5	8.8	441	US-11-056-355B-45282	Sequence 45282, A
18	74.5	8.8	463	US-11-056-355B-36354	Sequence 36354, A
19	74.5	8.8	463	US-11-056-355B-45281	Sequence 45281, A
20	74.5	8.8	1166	US-10-449-902-37528	Sequence 37528, A
21	73.5	8.6	466	US-10-953-349-18970	Sequence 18970, A
22	73.5	8.6	466	US-10-953-349-18969	Sequence 18969, A
23	73.5	8.6	565	US-10-471-571A-5038	Sequence 5038, Ap
24	71	8.4	378	US-10-953-349-12621	Sequence 32621, A
25	71	8.4	378	US-11-056-355B-64212	Sequence 64212, A

26	71	8.4	436	6	US-10-953-349-12620	Sequence 32620, A
27	71	8.4	436	6	US-11-056-355B-64211	Sequence 64211, A
28	71	8.4	461	7	US-10-953-349-12619	Sequence 32619, A
29	71	8.4	461	7	US-11-056-355B-64210	Sequence 64210, A
30	71	8.4	555	7	US-11-056-355B-79971	Sequence 79971, A
31	71	8.4	631	7	US-11-056-355B-79970	Sequence 79970, A
32	71	8.4	694	6	US-10-449-902-36372	Sequence 36372, A
33	71	8.4	864	7	US-11-056-355B-79969	Sequence 79969, A
34	70.5	8.3	352	7	US-11-056-355B-81843	Sequence 81843, A
35	70.5	8.3	720	6	US-10-449-902-51542	Sequence 51542, A
36	70	8.2	861	6	US-10-520-470-73	Sequence 73, Appl
37	69.5	8.2	653	6	US-10-449-902-52519	Sequence 52519, A
38	69	8.1	707	7	US-11-293-697-3241	Sequence 3241, Ap
39	69	8.1	923	6	US-10-449-902-41603	Sequence 41603, A
40	69	8.1	932	7	US-11-360-995-17	Sequence 17, Appl
41	69	8.1	932	7	US-11-360-995-18	Sequence 18, Appl
42	68.5	8.1	212	7	US-11-056-355B-4865	Sequence 4865, Ap
43	68.5	8.1	247	7	US-11-056-355B-56995	Sequence 56995, A
44	68.5	8.1	335	7	US-11-056-355B-4864	Sequence 4864, Ap
45	68.5	8.1	417	7	US-11-056-355B-4863	Sequence 4863, Ap

ALIGNMENTS

RESULT 1
US-10-511-937-2572
Sequence 2572, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2572
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2572

Query Match 100.0%; Score 850; DB 6; Length 162;

Best Local Similarity 100.0%; Pred. No. 6.3e-75; Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWIFLGTIVHKSSGQGDHMRIMROLIDIVOLKNYVNDLYPEF 60
DB 1 MRSSPGNMERIVICLWIFLGTIVHKSSGQGDHMRIMROLIDIVOLKNYVNDLYPEF 60
DB LPAPEDVETNCWAFSCFOAOLKSANTGNNEIIVASTIKLKRKPPSTNAGRORHRL 120
QY 61 LPAPEDVETNCWAFSCFOAOLKSANTGNNEIIVASTIKLKRKPPSTNAGRORHRL 120
DB 61 LPAPEDVETNCWAFSCFOAOLKSANTGNNEIIVASTIKLKRKPPSTNAGRORHRL 120
QY TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162
DB 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162
DB 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162

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RESULT 2
US-10-735-149-2
; Sequence 2, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Cover, Bruce L.
; APPLICANT: Cover, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-149-2

Query Match      100.0%; Score 850; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 LPAPDEVETNCESAFSCFOKAQLKSANTGNNERIINVSIIKLRKPPSTNAGRQGRHL 120
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QY      121 TCPSCDSEYKKPPEKPEFLERFKSLLOQKMIHQHLSRTHGSEDS 162
DB      121 TCPSCDSEYKKPPEKPEFLERFKSLLOQKMIHQHLSRTHGSEDS 162

RESULT 3
US-10-806-611-10
; Sequence 10, Application US/10806611
; Publication No. US20060159655A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Chin, Elaine Y.
; APPLICANT: Senices, Mayra
; APPLICANT: Young, Deborah A.
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
; FILE REFERENCE: 16158-013001
; CURRENT APPLICATION NUMBER: US/10/806,611
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 60/456,920
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-611-10

Query Match      100.0%; Score 850; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      121 TCPSCDSEYKKPPEKPEFLERFKSLLOQKMIHQHLSRTHGSEDS 162
DB      121 TCPSCDSEYKKPPEKPEFLERFKSLLOQKMIHQHLSRTHGSEDS 162

RESULT 4
US-11-429-276-2177
; Sequence 2177, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2177
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-2177

Query Match      100.0%; Score 850; DB 7; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      121 TCPSCDSEYKKPPEKPEFLERFKSLLOQKMIHQHLSRTHGSEDS 162
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; Sequence 2167, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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FILE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PFS64
CURRENT APPLICATION NUMBER: US/11/429, 276
CURRENT FILING DATE: 2006-05-08
PRIOR APPLICATION NUMBER: 10/775, 204
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: PCT/US02/40891
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 60/341, 811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360, 000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378, 950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398, 008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411, 355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414, 984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417, 611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420, 246
PRIOR FILING DATE: 2002-10-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2167
LENGTH: 742
TYPE: PRT
ORGANISM: Homo sapiens
US-11-429-276-2167

Query Match 83.4%; Score 708.5; DB 7; Length 742;
Best Local Similarity 90.1%; Pred. No. 2e-60;
Matches 136; Conservative 5; Mismatches 7; Indels 3; Gaps 1;
QY 15 LMTVFLGLTVHKS---SQGDHRMIRMRQLIDVDLQKYNVNDLVPEFLPAPEDVETNC 71
DB 7 ISLFLFSSAYSRSIDKRGQDRHMRQLIDVDLQKYNVNDLVPEFLPAPEDVETNC 66
QY 72 EWSAFSCFOKQKLSANTGNNERIINVSIKLKRRKPPSTNAGRQKRLTGPCDSYEKK 131
DB 67 EWSAFSCFOKQKLSANTGNNERIINVSIKLKRRKPPSTNAGRQKRLTGPCDSYEKK 126
QY 132 PKKEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 127 PKKEFLERFKSLQKMIHQHLSRTHGSEDS 157

RESULT 6
US-10-735-149-28
Sequence 28, Application US/10735149
Publication No. US20060134754A1
GENERAL INFORMATION:
APPLICANT: Chan, Chung
APPLICANT: Zamosc, Bruce L.
APPLICANT: Covert, Douglas C.
APPLICANT: Liu, Hong Y.
APPLICANT: De Jongh, Karen S.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
FILE REFERENCE: 02-12
CURRENT APPLICATION NUMBER: US/10/735, 149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 134
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: optimized IL-21
US-10-735-149-28

Query Match 83.1%; Score 706; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 4.2e-61;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 QGDHRMIRMRQLIDVDLQKYNVNDLVPEFLPAPEDVETNCWSAFSCFOKQKLSANT 89
DB 2 QGDHRMIRMRQLIDVDLQKYNVNDLVPEFLPAPEDVETNCWSAFSCFOKQKLSANT 61
QY 90 GNNERIINVSIKLKRRKPPSTNAGRQKRLTGPCDSYEKKPKPEFLERFKSLQKMIH 149
DB 62 GNNERIINVSIKLKRRKPPSTNAGRQKRLTGPCDSYEKKPKPEFLERFKSLQKMIH 121
QY 150 QHLSRTHGSEDS 162
DB 122 QHLSRTHGSEDS 134

RESULT 7
US-10-806-611-2
Sequence 2, Application US/10806611
Publication No. US20060159655A1
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806, 611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456, 920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 131
TYPE: PRT
ORGANISM: Homo sapiens
US-10-806-611-2

Query Match 81.8%; Score 695; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.8e-60;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 QDRHMIRMRQLIDVDLQKYNVNDLVPEFLPAPEDVETNCWSAFSCFOKQKLSANTGN 91
DB 1 QDRHMIRMRQLIDVDLQKYNVNDLVPEFLPAPEDVETNCWSAFSCFOKQKLSANTGN 60
QY 92 NERIINVSIKLKRRKPPSTNAGRQKRLTGPCDSYEKKPKPEFLERFKSLQKMIHQH 151
DB 61 NERIINVSIKLKRRKPPSTNAGRQKRLTGPCDSYEKKPKPEFLERFKSLQKMIHQH 120
QY 152 LSSRTHGSEDS 162
DB 121 LSSRTHGSEDS 131

RESULT 8
US-10-806-611-12
Sequence 12, Application US/10806611
Publication No. US20060159655A1
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806, 611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456, 920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 131
TYPE: PRT
ORGANISM: Homo sapiens
US-10-806-611-12

FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 122
TYPE: PRT
ORGANISM: Bos taurus
US-10-806-611-12

Query Match 61.6%; Score 524; DB 6; Length 122;
Best Local Similarity 80.3%; Pred. No. 1.5e-43;
Matches 98; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 32 QDRHMIMRQLIDIVDOLKNVNDLVEPEFLPAPEDVETNCMSAFSCFOKAQLKSANTGN 91
DB 1 QDRFLIRLRLDIDVDOLKNVNDLDEPEFLPAPEDVGRHCHRSASFSCFOKAQLKSANNGD 60
QY 92 NERLIVNSIKKLKRRKPPSTNAGRQKRLTCSDCSYEKRPKEFLERFKSLQKMIHQH 151
DB 61 NEKILNITLQKLRKLDPATWTGRQKHVETPCSDSYEKRPKEFLERFKSLQKMIHQH 120

QY 152 LS 153
DB 121 LS 122

RESULT 9
US-10-806-611-13
Sequence 13, Application US/10806611
Publication No. US20060159655A1
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 146
TYPE: PRT
ORGANISM: Mus musculus
US-10-806-611-13

Query Match 57.2%; Score 486; DB 6; Length 146;
Best Local Similarity 63.0%; Pred. No. 8.9e-40;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVLCMWIFLGTLVHKSSSGQDRHMIMRQLIDIVDOLKNVNDLVEPEFLPAPEDV 67
DB 1 MERLIVLCVVIPLGTVAHKSSPGQDRHILRLRLDIDVEGLKIYENDLDEPEFLSAPQDV 60
QY 68 ETNCMSAFSCFOKAQLKSANTGNNERLIVNSIKKLKRRKPPSTNAGRQKRLTCSDCS 127
DB 61 KGHCEHAFAFCFOKAKKPPSPGNKTFIIDLVAQLRRRLPARRGKKQKXIAKPCSCDS 120
QY 128 YEKKPKPEFLERFKSLQKMIHQHLS 153
DB 121 YEKTPKEFLERLKLMLQKMIHQHLS 146

RESULT 10
US-10-806-611-4

Sequence 4, Application US/10806611
Publication No. US20060159655A1
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 122
TYPE: PRT
ORGANISM: Mus musculus
US-10-806-611-4

Query Match 46.4%; Score 394; DB 6; Length 122;
Best Local Similarity 62.0%; Pred. No. 5.7e-31;
Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 33 DRHMIMRQLIDIVDOLKNVNDLVEPEFLPAPEDVETNCMSAFSCFOKAQLKSANTGN 92
DB 2 DRLIRLRLDIDVEQLKIYENDLDEPEFLSAPQDVGRHCHRSASFSCFOKAQLKSPNGNN 61
QY 93 ERLIVNSIKKLKRRKPPSTNAGRQKRLTCSDCSYEKRPKEFLERFKSLQKMIHQH 152
DB 62 KTFIIDLVAQLRRRLPARRGKKQKXIAKPCSDSYEKRPKEFLERFKSLQKMIHQH 121

QY 153 S 153
DB 122 S 122

RESULT 11
US-10-511-937-2499
Sequence 2499, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2499
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2499

Query Match 11.7%; Score 99.5; DB 6; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.025;

	Matches	30;	Conservative	23;	Mismatches	44;	Indels	15;	Gaps	5
Qy	43	IDIVDLQNYNDI	PEEP-----	LEAPDEVTNC	CEMSAFSCP-----	OKAQLCSANT	GNNE	93		
		::: ::	::: ::	::: ::	::: ::	::: ::	::: ::			
Db	51	VNVISDEKK	-IEDIIQSMHIDAT	LVTESGDVHPS	CKVTAMKCFLEI	QVTSIESG	DASTHD	109		
Qy	94	RIINVSTCKLRKRP	STNAGRRÖKRL	CPSCSDSYEKRR	PKPEFELR	PFSLQKMH	149			
		::: ::	::: ::	::: ::	::: ::	::: ::	::: ::			
Db	110	TVENDIIT--	LMANNSSNGNTES---	GCKEEBELEKNIK	REFLOSFNHIV	GMFIN	160			

```

RESULT 12
US-11-429-276-1162
Sequence 1162, Application US/11429276
Publication No. US20060194735A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PEP564
CURRENT APPLICATION NUMBER: US/11/429,276
CURRENT FILING DATE: 2006-05-08
PRIOR APPLICATION NUMBER: 10/775,204
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: PCT/US02/40891
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1162
LENGTH: 605
TYPE: PRT
ORGANISM: Xenopus laevis
US-11-429-276-1162

```

```

Query Match 9.6%; Score 82; DB 7; Length 605;
Best Local Similarity 24.2%; Pred No. 6.3;
Matches 38; Conservative 19; Mismatches 50; Indels 50; Gaps 6

QY 44 DIVDLKNVYNDLVDFE-----LPABEDYETNCWMSAFSCF---QKAQLKSAN 88
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 EINDPAKSCINDPTECEKCPVGTLPFDKLCADPAVGNNWEMSEKCCAKQDPBRAQCFKHA 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 89 TGNRRIT---NVSIKKLRK-----PPTNNAQRQKRLTCS 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 RDHEHTSIKPEEPECKLKEHPDDL$AFIIEARNHEDLYP$PAVLATLKYHNKLA$HC 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 125 CDSYEKKPPEKLEFRKSLQGMQH$SSRTHG$SD 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 CEEEDKE--KCFSEKMKQLMK-----Q$H$TSD 215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 13
US-11-251-208-77
; Sequence 77, Application US/11251208
; Publication No. US20060317043A1
; GENERAL INFORMATION:
; APPLICANT: Puzio, Piotr

```

1  APPLICANT: Chardonnens, Agnes
2  APPLICANT: Shirley, Amber
3  APPLICANT: Wang, Xi-Qing
4  APPLICANT: Sarría-Millan, Rodrigo
5  APPLICANT: McKersie, Bryan
6  APPLICANT: Chen, Ruoying
7  TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC
8  TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED
9  TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS
10 FILE REFERENCE: 1311-00015-US
11 CURRENT APPLICATION NUMBER: US/11/251,208
12 CURRENT FILING DATE: 2005-10-14
13 PRIOR APPLICATION NUMBER: PCT/US2004/011868
14 PRIOR FILING DATE: 2004-04-15
15 PRIOR APPLICATION NUMBER: EP 03008080.8
16 PRIOR FILING DATE: 2003-04-15
17 PRIOR APPLICATION NUMBER: EP 03009728.1
18 PRIOR FILING DATE: 2003-05-02
19 PRIOR APPLICATION NUMBER: EP 03016672.2
20 PRIOR FILING DATE: 2003-08-01
21 PRIOR APPLICATION NUMBER: EP 03022225.1
22 PRIOR FILING DATE: 2003-09-30
23 NUMBER OF SEQ ID NOS: 852
24 SOFTWARE: Patentln version 3.3
25 SEQ ID NO 77
26 LENGTH: 864
27 TYPE: PRT
28 ORGANISM: Saccharomyces cerevisiae
29 US-11-208-77

```

```

Query Match          9.0%; Score 76.5; DB 7; Length 864;
Best Local Similarity 12.5%; Pred. No. 33;
Matches      43; Conservative 22; Mismatches 59; Indels 67; Gaps 8

QY      2 RSSFGNNRIYIC---LMIPLGLTVHKSSQSGODRMIRKQRLDIDVDQKYNVDLV 57
Db       5 RCGPKN---VLCEPFLQSLFESKRLNK-----RKYTLQTEDE-KNNMGSL 49
QY      58 PEPLPAPEDEVETNCWESAFSCFOKAQLSANTGNNNRIIIVNSIKKLKKRPSTNAGRROK 117
Db       50 KKKIITPEDEV-----FKLAQLNEFSNTLKERLHNTK-----SVNSDGHQS 90
QY      118 HRLTQPCSDSYEKPKP-----EFLERKSLLOKMIHQ----- 150
Db       91 NSIAPISDSISNNVNTKTSVVPNEEKSKNLSLDLIHSSFLEKMDHLVPKVIERRVADDITL 150
QY      151 --HLSSRTGGS 159
Db       151 AKNLFDKRSN 161

```

```

RESULT 14
US-11-056-355B-36356
; Sequence 36356, Application US/11056355B
; Publication No. US2006015028A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OR INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 36356
; LENGTH: 431
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(431)

```

OTHER INFORMATION: Ceres Seq. ID no. 13575998
US-11-056-355B-36356

Query Match 8.8%; Score 74.5; DB 7; Length 431;
Best Local Similarity 21.8%; Pred. No. 22;
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY 34 RHMIRMQLDIDVQKXVYNDLVPEFLPAPEDVETNCWSAFSCFOKAOLKSANTGNN 93
DB 220 KYKLAARKFLDVNPGLGNSYNEVI-APQDIATYGGLCALASFDRSEIK-----Q 267
QY 94 RII-NVSIKIKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPPKEFLERFKSLQKMIHQH 151
DB 268 KVIDNINFRNPELVDPVRELINDFYSSRYASC-----LEYLASIKSNLLDIDH 318

RESULT 15

US-11-056-355B-45283
Sequence 45283, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ. ID NOS: 119966
SEQ. ID NO 45283
LENGTH: 431
TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1)-(431)
OTHER INFORMATION: Ceres Seq. ID no. 13575998
US-11-056-355B-45283

Query Match 8.8%; Score 74.5; DB 7; Length 431;
Best Local Similarity 21.8%; Pred. No. 22;
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY 34 RHMIRMQLDIDVQKXVYNDLVPEFLPAPEDVETNCWSAFSCFOKAOLKSANTGNN 93
DB 220 KYKLAARKFLDVNPGLGNSYNEVI-APQDIATYGGLCALASFDRSEIK-----Q 267
QY 94 RII-NVSIKIKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPPKEFLERFKSLQKMIHQH 151
DB 268 KVIDNINFRNPELVDPVRELINDFYSSRYASC-----LEYLASIKSNLLDIDH 318

Search completed: September 7, 2006, 12:58:48
Job time : 10.9514 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 7, 2006, 12:39:36 : Search time 222.886 Seconds
(without alignments)
1103.626 Million cell updates/sec

Title: US-10-659-684-115

Perfect score: 2958
Sequence: 1 MPRGMAAPLLLLLLQGSGWC.....YLRQWVIPPPLSSPSPQAS 538

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2958	100.0	538	2	AAV27450 Human MU-
2	2958	100.0	538	3	AAV27450 Human MU-
3	2958	100.0	538	3	AAV27450 Human MU-
4	2958	100.0	538	3	AAV27450 Human MU-
5	2958	100.0	538	3	AAV27450 Human MU-
6	2958	100.0	538	3	AAV27450 Human MU-
7	2958	100.0	538	3	AAV27450 Human MU-
8	2958	100.0	538	3	AAV27450 Human MU-
9	2958	100.0	538	3	AAV27450 Human MU-
10	2958	100.0	538	3	AAV27450 Human MU-
11	2958	100.0	538	3	AAV27450 Human MU-
12	2958	100.0	538	3	AAV27450 Human MU-
13	2958	100.0	538	3	AAV27450 Human MU-
14	2958	100.0	538	3	AAV27450 Human MU-
15	2958	100.0	538	3	AAV27450 Human MU-
16	2958	100.0	538	3	AAV27450 Human MU-
17	2958	100.0	538	3	AAV27450 Human MU-
18	2958	100.0	538	3	AAV27450 Human MU-
19	2958	100.0	538	3	AAV27450 Human MU-
20	2958	100.0	538	3	AAV27450 Human MU-
21	2958	100.0	538	3	AAV27450 Human MU-
22	2958	100.0	538	3	AAV27450 Human MU-
23	2958	100.0	538	3	AAV27450 Human MU-

24	2958	100.0	538	8	ADS19027	AdS19027 Mature hu
25	2958	100.0	538	8	ADS41470	AdS41470 Human hae
26	2958	100.0	538	8	ADV96468	Adv96468 Human hae
27	2958	100.0	538	9	ADY17832	AdY17832 PRO polyp
28	2958	100.0	538	9	ADY17690	AdY17690 PRO polyp
29	2958	100.0	538	9	ADY20089	AdY20089 PRO polyp
30	2958	100.0	538	9	ADY54732	AdY54732 Human zai
31	2958	100.0	538	9	ADY21785	AdY21785 Human can
32	2958	100.0	538	9	ADY212787	AdY212787 Human can
33	2958	100.0	538	9	ADZ20509	AdZ20509 Human int
34	2958	100.0	538	10	AEI19676	AeI19676 Human int
35	2958	100.0	538	10	AEI05256	AeI05256 Human IL-
36	2951	99.8	538	3	AAV94304	AAV94304 Human HNO
37	2951	99.8	538	4	AAU08728	AAU08728 Human HNO
38	2933	99.2	538	4	AAE02459	AAE02459 Human DNA
39	2905	98.2	538	3	AAV69888	AAV69888 Mouse hae
40	2851	96.4	519	9	ADY54825	AdY54825 Human hae
41	2817	95.2	568	3	AAV94305	AAV94305 Human HNO
42	2817	95.2	568	4	AAE02457	AAE02457 Human DNA
43	2817	95.2	568	4	AAU08729	AAU08729 Human HNO
44	2817	95.2	568	5	AAE13738	AeI13738 Human sol
45	1899.5	64.2	361	3	AAV69883	AAV69883 Human hae

ALIGNMENTS

RESULT 1
ID AAV27450 standard; protein; 538 AA.
XX
AC AAV27450;
XX
DT 26-NOV-1999 (first entry)
XX
DE Human MU-1 hematopoietin receptor protein.
XX
KW MU-1 hematopoietin receptor protein; e MU-1 protein; gene therapy;
KW cell proliferation; cytokine production; immune response; cancer;
KW autoimmune disease; transplant rejection; hematopoiesis; anemia;
KW gene mapping; nutritional supplement; human.
XX
OS Homo sapiens.
XX
PN W09947675-A1.
XX
PD 23-SEP-1999.
XX
PF 17-MAR-1999; 99WC-US005854.
XX
PR 17-MAR-1998; 98US-00040005.
XX
PA (GEMV) GENETICS INST INC.
XX
PI Donaldson D, Ungar M;
XX WPI; 1999-562115/47.
XX DR N-PSDB; AA07535.
XX PT New nucleic acid encoding the MU-1 hematopoietin receptor protein, used
XX for treating e.g. cancer, autoimmune disease or abnormal hematopoiesis.
XX PS
XX Claim 9; Page 33-35; 37pp; English.
XX
XX This represents a MU-1 hematopoietin receptor protein. The protein can be
XX produced by standard recombinant methodology. The MU-1 protein has the
XX biological activity of the MU-1 hematopoietin receptor superfamily chain.
XX It is used to screen for specific binding agents, to raise specific
XX antibodies; as assay reagents, tissue markers etc. and therapeutically
XX (optionally) expressed from the MU-1 gene by gene therapy. Many possible
XX activation/uses of the MU-1 protein are described without supporting
XX evidence, e.g. they regulate cell proliferation and differentiation,
XX induce production of cytokines, stimulate or suppress an immune response

CC (e.g. for treating immune deficiency of any etiology, cancer or
CC autoimmune disease, and for preventing transplant rejection) and regulate
CC of hematopoiesis, e.g. for treating anemia. The MU-1 gene is used as a
CC research reagent, for recombinant production of the protein, as tissue or
CC molecular weight marker, for gene mapping; for production of anti-DNA or
CC anti-protein antibodies etc. The MU-1 protein and the nucleic acids are
CC also useful as nutritional supplements or sources and the antibodies can
CC be used therapeutically, as assay reagents and for affinity purification
XX
SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.5e-240; Indels 0; Gaps 0;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAPLPLLLLLLOGMGCPDLVCYTDYLOTVCILEMNNLHPSTLTTLTWMODQYEELKD 60
DB 1 MPRGMAPLPLLLLLLOGMGCPDLVCYTDYLOTVCILEMNNLHPSTLTTLTWMODQYEELKD 60
QY 61 EATSCSLHRSAHNATHATYTCMDVFFHMADDFISVNTTQSGNYSQECGFFLAESIKP 120
DB 61 EATSCSLHRSAHNATHATYTCMDVFFHMADDFISVNTTQSGNYSQECGFFLAESIKP 120
QY 121 APPNNVTVTSSGOYNISWRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
DB 121 APPNNVTVTSSGOYNISWRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
QY 181 RSVSLPLPERKDSYELQVRAGMPGSSYQGTWSEMSDVIPTQSEELKEGNPHLL 240
DB 181 RSVSLPLPERKDSYELQVRAGMPGSSYQGTWSEMSDVIPTQSEELKEGNPHLL 240
QY 241 LLLLVIVIFAPFWSLKTHTPLRLMKKIWAVSPERFFMPLKYKSGDPKKVGAFFTGSS 300
DB 241 LLLLVIVIFAPFWSLKTHTPLRLMKKIWAVSPERFFMPLKYKSGDPKKVGAFFTGSS 300
QY 301 LELGPMSEVPSTLEVYSCHPPSPAKRLQTLQEPALVELVSDGVPRFPMPAONSGG 360
DB 301 LELGPMSEVPSTLEVYSCHPPSPAKRLQTLQEPALVELVSDGVPRFPMPAONSGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDDAGLESPGLEDDPLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDDAGLESPGLEDDPLD 420
QY 421 AGTTVLSGCGVSAGSPGLGPGLSLDRKPLADGEMAGCLPMGGRSPGCVSESEAGS 480
DB 421 AGTTVLSGCGVSAGSPGLGPGLSLDRKPLADGEMAGCLPMGGRSPGCVSESEAGS 480
QY 481 PLAGLMDTPDPSGVSGSPVCECDFTSPGDEGPPRSYLQWVYIPPLSSPGQAS 538
DB 481 PLAGLMDTPDPSGVSGSPVCECDFTSPGDEGPPRSYLQWVYIPPLSSPGQAS 538

RESULT 2

AA18634
ID AA18634 standard; protein; 538 AA.

AC AA18634;

DT 22-JAN-2001 (first entry)

DE A human zalphall ligand polypeptide.

XX zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;

XX tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

XX Homo sapiens.

PN M0200053761-A2.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000MO-US006067.

PR 09-MAR-1999; 99US-00264908.
PR 11-MAR-1999; 99US-00265992.
PR 01-JUN-1999; 99US-0142013P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX WPI; 2000-565600/52.
DR N-PSDB; AAA75557.
XX
XX New human cytokine, designated zalphall ligand, useful for stimulating
PT the proliferation and/or development of hematopoietic cells in vitro and
PT in vivo, and for treating tumorigenesis.
XX
XX Disclosure; Page 255-256; 256pp; English.

CC The present sequence represents a human zalphall ligand polypeptide,
CC which is a cytokine. The zalphall ligand is useful for stimulating the
CC proliferation and development of haematopoietic cells in vitro and in
CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
CC for cloning the zalphall gene. The zalphall ligand is useful for treating
CC tumorigenesis. A zalphall ligand-saporin fusion toxin may be used for
CC treating leukaemia and lymphomas. Antagonists against zalphall ligand
CC are useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalphall ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphall ligand
CC genetic defect
XX

SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.5e-240; Indels 0; Gaps 0;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAPLPLLLLLLOGMGCPDLVCYTDYLOTVCILEMNNLHPSTLTTLTWMODQYEELKD 60
DB 1 MPRGMAPLPLLLLLLOGMGCPDLVCYTDYLOTVCILEMNNLHPSTLTTLTWMODQYEELKD 60
QY 61 EATSCSLHRSAHNATHATYTCMDVFFHMADDFISVNTTQSGNYSQECGFFLAESIKP 120
DB 61 EATSCSLHRSAHNATHATYTCMDVFFHMADDFISVNTTQSGNYSQECGFFLAESIKP 120
QY 121 APPNNVTVTSSGOYNISWRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
DB 121 APPNNVTVTSSGOYNISWRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
QY 181 RSVSLPLPERKDSYELQVRAGMPGSSYQGTWSEMSDVIPTQSEELKEGNPHLL 240
DB 181 RSVSLPLPERKDSYELQVRAGMPGSSYQGTWSEMSDVIPTQSEELKEGNPHLL 240
QY 241 LLLLVIVIFAPFWSLKTHTPLRLMKKIWAVSPERFFMPLKYKSGDPKKVGAFFTGSS 300
DB 241 LLLLVIVIFAPFWSLKTHTPLRLMKKIWAVSPERFFMPLKYKSGDPKKVGAFFTGSS 300
QY 301 LELGPMSEVPSTLEVYSCHPPSPAKRLQTLQEPALVELVSDGVPRFPMPAONSGG 360
DB 301 LELGPMSEVPSTLEVYSCHPPSPAKRLQTLQEPALVELVSDGVPRFPMPAONSGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDDAGLESPGLEDDPLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDDAGLESPGLEDDPLD 420
QY 421 AGTTVLSGCGVSAGSPGLGPGLSLDRKPLADGEMAGCLPMGGRSPGCVSESEAGS 480
DB 421 AGTTVLSGCGVSAGSPGLGPGLSLDRKPLADGEMAGCLPMGGRSPGCVSESEAGS 480

Qy 481 PLGLMDPTDPSGFGVSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPQAS 538
 Db 481 PLGLMDPTDPSGFGVSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPQAS 538

RESULT 3

AAV45031
 ID AAV45031 standard; protein; 538 AA.

AAV45031;

31-MAY-2000 (first entry)

DE HUMAN Orphan Cytokine Receptor 10 (OCR10) -A polypeptide.

KM Human; Orphan Cytokine Receptor 10-A; OCR10-A; cytokine; screen; cognate ligand; treatment; endocrine disorder; immune disorder.

OS Homo sapiens.

PN WO200008152-A1.

PD 17-FEB-2000.

PF 16-JUL-1999; 99WO-US016060.

PR 04-AUG-1998; 98US-00128820.

PA (REG-) REGENERON PHARM INC.

PI Maslakowski PJ, Morris J, Valenzuela DM;

DR WPI; 2000-205707/18.

XX N-PSDB; AAZ50748.

PT New HUMAN orphan cytokine receptors 10 and 10-A useful for screening for drugs e.g. receptor agonists that may mediate survival and differentiation in cells naturally expressing the receptor and for screening for cognate ligands.

PS Example 10; Page 39-41; 54pp; English.

XX The present sequence is that of HUMAN Orphan Cytokine Receptor 10-A (OCR10-A) polypeptide. It is expressed at high levels in spleen, thymus, peripheral blood leucocytes and lymph nodes and moderately in heart and placenta. It has a role in immune system and cytokine function. It is useful in screening for cognate ligands or drugs that mediate survival and differentiation of cells expressing this receptor. Modified HUMAN OCR10-A or its agonist can be used in the treatment of endocrine or immune disorders

XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 3; Length 538;

Best Local Similarity 100.0%; Pred. No. 7, 5e-240; Indels 0; Gaps 0; Matches 538; Conservative 0; Mismatches 0;

Qy 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDYEEELKD 60
 Db 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDYEEELKD 60
 Qy 61 EATSCSLHRSANHTATYTCMDVFFPMADDFSVNITDQSGVSGCGSFLLAESIKP 120
 Db 61 EATSCSLHRSANHTATYTCMDVFFPMADDFSVNITDQSGVSGCGSFLLAESIKP 120
 Qy 121 APPNNVVTSGQVNIWSRSDYEDPAFMYLKGKLYEELQYNRRDDPMAVSPRRKLISVDS 180
 Db 121 APPNNVVTSGQVNIWSRSDYEDPAFMYLKGKLYEELQYNRRDDPMAVSPRRKLISVDS 180
 Qy 181 RSVSLLPLPERKDSYELQVRAGPMPSGYQGTWSEMSDPVIFOTOSSELKEGNNPHLL 240
 Db 181 RSVSLLPLPERKDSYELQVRAGPMPSGYQGTWSEMSDPVIFOTOSSELKEGNNPHLL 240

Qy 241 LLLVIVIFDAPMSLKTPIMLRLMKKIWAVSPERFEMPLYKGGSGDFKKWVGAPEFTGSS 300
 Db 241 LLLVIVIFDAPMSLKTPIMLRLMKKIWAVSPERFEMPLYKGGSGDFKKWVGAPEFTGSS 300
 Qy 301 LELGPMSPVSTLEVYSCHPSPSPAKRLQTLQEPALVESDGVKPSFMP7AQN5G 360
 Db 301 LELGPMSPVSTLEVYSCHPSPSPAKRLQTLQEPALVESDGVKPSFMP7AQN5G 360
 Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCWPCSCEDDGPALDLDALBSPGLDEPLD 420
 Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCWPCSCEDDGPALDLDALBSPGLDEPLD 420
 Qy 421 AGTTVSCGVASGSPGLGPIGLDRLKPLADGEMDAGLPMGGRSPGVSE5AGS 480
 Db 421 AGTTVSCGVASGSPGLGPIGLDRLKPLADGEMDAGLPMGGRSPGVSE5AGS 480
 Qy 481 PLGLMDPTDPSGFGVSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPQAS 538
 Db 481 PLGLMDPTDPSGFGVSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPQAS 538

RESULT 4

AAV69886
 ID AAV69886 standard; protein; 538 AA.

AAV69886;

24-MAY-2000 (first entry)

DE Human haemopoietin receptor family member NR8gamma.

KM Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder.

OS Homo sapiens.

PN WO9967290-A1.

PD 29-DEC-1999.

PF 23-JUN-1999; 99WO-JP003351.

PR 24-JUN-1998; 98JP-00214720.

PR 19-OCT-1998; 98JP-00297409.

PA (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.

PI Nomura H, Maeda M;

DR WPI; 2000-116933/10.

DR N-PSDB; AAZ59240.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders.

PS Claim 4; Fig 9-10; 176pp; Japanese.

XX This sequence represents a novel haemopoietin receptor protein family NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders

XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 3; Length 538;

Best Local Similarity 100.0%; Pred. No. 7, 5e-240; Indels 0; Gaps 0; Matches 538; Conservative 0; Mismatches 0;

Qy 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDYEEELKD 60
 Db 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDYEEELKD 60
 Qy 61 EATSCSLHRSANHTATYTCMDVFFPMADDFSVNITDQSGVSGCGSFLLAESIKP 120

Db 61 EATSCSLHRSAHNATHATYTCCHMDVFFHMADDFISVNTTDSQGNYSQECGSFLLAESIKP 120
Qy 121 APPENVTVTFSSGQYNI SMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
Db 121 APPENVTVTFSSGQYNI SMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
Qy 181 RSVSLPLLEFRKQSSYELQVRAGPMPGSSYQGTWSEMSDPVIFQTSBELKEGMNPHLL 240
Db 181 RSVSLPLLEFRKQSSYELQVRAGPMPGSSYQGTWSEMSDPVIFQTSBELKEGMNPHLL 240
Qy 241 LLLLVIVIFIPAFMSLKTTHPLRLMKKIWA VSPERFPMPLKKGSGDFKKVVGAPFTGSS 300
Db 241 LLLLVIVIFIPAFMSLKTTHPLRLMKKIWA VSPERFPMPLKKGSGDFKKVVGAPFTGSS 300
Qy 301 LEIGPMSPEVPSTLEVYSCHPPRSPAKRLQLTIELQEPALVESQGVKPSFWPTAQNSSG 360
Db 301 LEIGPMSPEVPSTLEVYSCHPPRSPAKRLQLTIELQEPALVESQGVKPSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSI DTIVTVLDAEGPCTWPCSCEDDGYPALDLAGLESPGLEPDL 420
Db 361 SAYSEERDRPYGLVSI DTIVTVLDAEGPCTWPCSCEDDGYPALDLAGLESPGLEPDL 420
Qy 421 AGTVLSCGCVSAGSPGLGPGLSLDRKPLADGEDMAGCLPMGGRSPGVSESEAGS 480
Db 421 AGTVLSCGCVSAGSPGLGPGLSLDRKPLADGEDMAGCLPMGGRSPGVSESEAGS 480
Qy 481 PLAGLMDTFDPSGFGVSDCSSPVECDFTSPGDEGPFRSYLRQWVVIPLPLSSPGQAS 538
Db 481 PLAGLMDTFDPSGFGVSDCSSPVECDFTSPGDEGPFRSYLRQWVVIPLPLSSPGQAS 538

RESULT 5
AAV79312
ID AAV79312 standard; protein; 538 AA.
XX AAV79312;
XX 18-JUL-2000 (first entry)
XX Human cytokine receptor zalphall.
XX DE Human cytokine receptor zalphall.
XX KW Cytokine receptor; zalphall; human; chromosome 16p11.1; apoptosis;
KW signal transduction; growth factor; cancer; tumour; infection;
KW immunosuppressive; immunostimulant; autoimmune disease; leukaemia;
KW lymphoma; transplant rejection; therapy; diagnosis.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /note= "signal peptide"
FT Protein 20..538 /note= "mature protein; a polypeptide comprising the mature protein is specifically claimed in Claim 27(d)"
FT Domain 20..237 /note= "cytokine-binding domain; a polypeptide comprising this domain is specifically claimed in Claim 27(a)"
FT Domain 192..202 /note= "penultimate strand region"
FT Region 214..218 /note= "MSXMS motif"
FT Domain 238..255 /note= "transmembrane domain"
FT Domain 256..538 /note= "intracellular signalling domain; a polypeptide comprising this domain is specifically claimed in Claim 27(c)"
FT Region 267..273 /note= "Box I signalling site"
FT Region 301..304 /note= "Box II signalling site"
XX

PN WO200017235-A2.
XX 30-MAR-2000.
XX 23-SEP-1999; 99WO-US022149.
XX 23-SEP-1998; 98US-00159254.
XX 09-MAR-1999; 99US-00265117.
XX 06-JUL-1999; 99US-00347930.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;
XX WPI: 2000-292825/25.
XX N-PSDB; AA294533, AA294534.
XX Novel nucleic acid encoding zalphall polypeptide, useful for treating
PT e.g. viral infection or tumors, and for identifying ligands that
PT stimulate cell proliferation.
XX Claim 27(e); Page 148-149; 190pp; English.
XX
XX The present sequence is that of zalphall, a novel human class I cytokine
CC receptor that may be involved in an apoptotic cellular pathway, or is a
CC cell-cell signalling molecule, growth factor receptor, or extracellular
CC matrix associated protein with growth factor hormone activity. The
CC sequence was deduced from a cDNA clone (see AA294533) isolated from a
CC spinal cord library. Polypeptides comprising amino acids 20-237, 20-255,
CC 256-538, 20-538 and 1-538 of the present sequence are claimed. Zalphall
CC is expressed in lymph node, peripheral blood leucocytes, spleen and
CC thymus. The mRNA is also abundant in the Raji cell line (ATCC CCL 86)
CC derived from Burkitt's lymphoma. Zalphall polypeptides, and fusion
CC proteins, including chem, can be obtained by expression in recombinant
CC host cells. They are used: to detect ligands (also ligand agonists and
CC antagonists) that stimulate proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells, in vitro or in vivo, e.g. as
CC a replacement for serum in culture media; in soluble form to block ligand
CC activity (direct antagonists) and to detect ligand-expressing cancers; to
CC raise specific antibodies; and for purification of cognate ligands.
CC Agonistic ligands may stimulate cell-mediated immunity, e.g. for treating
CC (viral) infections associated with immunosuppression, improving the
CC activity of vaccines, suppressing tumours, treating leukaemia and
CC improving T-cell regeneration after bone marrow transplant. Antagonists
CC are useful as immunosuppressants, e.g. in the treatment of autoimmune
CC disease (e.g. rheumatoid arthritis, multiple sclerosis, diabetes), to
CC prevent transplant rejection and to treat T-cell leukemia or lymphoma
XX
XX Sequence 538 AA:
XX
XX Query Match 100.0%; Score 2958; DB 3; Length 538;
XX Best Local Similarity 100.0%; Pred. No. 7, 5e-240; Indels 0; Gaps 0;
XX Matches 538; Conservative 0; Mismatches 0;
Qy 1 MPRGMAPLILLLLGGMGCPDLVCYDYDQYICILEMMNLHPSTLTLMQOYBELKD 60
Db 1 MPRGMAPLILLLLGGMGCPDLVCYDYDQYICILEMMNLHPSTLTLMQOYBELKD 60
Qy 61 EATSCSLHRSAHNATHATYTCCHMDVFFHMADDFISVNTTDSQGNYSQECGSFLLAESIKP 120
Db 61 EATSCSLHRSAHNATHATYTCCHMDVFFHMADDFISVNTTDSQGNYSQECGSFLLAESIKP 120
Qy 121 APPENVTVTFSSGQYNI SMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
Db 121 APPENVTVTFSSGQYNI SMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
Qy 181 RSVSLPLLEFRKQSSYELQVRAGPMPGSSYQGTWSEMSDPVIFQTSBELKEGMNPHLL 240
Db 181 RSVSLPLLEFRKQSSYELQVRAGPMPGSSYQGTWSEMSDPVIFQTSBELKEGMNPHLL 240
Qy 241 LLLLVIVIFIPAFMSLKTTHPLRLMKKIWA VSPERFPMPLKKGSGDFKKVVGAPFTGSS 300
Db 241 LLLLVIVIFIPAFMSLKTTHPLRLMKKIWA VSPERFPMPLKKGSGDFKKVVGAPFTGSS 300

QY 301 LELGPMSPVSTLEVTSCHPSPSPAKRLQTLTELOEPAELVESDGVKPSWPTAQNNGG 360
DB 301 LELGPMSPVSTLEVTSCHPSPSPAKRLQTLTELOEPAELVESDGVKPSWPTAQNNGG 360
QY 361 SAYSEERDRPYGLVSDIVTVTLDAEGPCTWPCSCEDDGYPALDDAGLESPGLEDPLLD 420
DB 361 SAYSEERDRPYGLVSDIVTVTLDAEGPCTWPCSCEDDGYPALDDAGLESPGLEDPLLD 420
QY 421 AGTTLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTTLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGQAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGQAS 538

RESULT 6
AAB48001
ID AAB48001 standard; protein, 538 AA.
AC AAB48001;
XX AAB48001;
XX 19-MAR-2001 (first entry)
DT Human IL-9/IL-2 receptor-like 16445 protein.
DE Human IL-9/IL-2 receptor-like 16445 protein.
XX Interleukin-9; IL-9; IL-2 receptor; 16445 protein; inflammatory;
KW T-lymphocyte-related disorder; antiarthritic; antipsoriatic; human;
KW immunosuppressive; antidiabetic; antiallergic; antithyroid; cytostatic;
KW antidiabetic; nephrotropic; gene therapy.
XX Homo sapiens.
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT Peptide 1..19
FT Protein /note= "signal peptide"
FT Protein 20..538
FT Protein /note= "mature protein"

W0200069880-A1.
23-NOV-2000.
18-MAY-2000; 2000MO-US013687.
PF 18-MAY-1999; 99US-00333913.
XX 18-MAY-1999;
PR (MILL-) MILLENNIUM PHARM INC.
PA Hodge MR;
PI WPI; 2001-016209/02.
DR N-PSDB; AAC84147.
XX
XX Novel interleukin-9/interleukin-2 receptor-like polypeptides useful for
PT diagnosis and treatment immune, inflammatory and respiratory disorders
PT and in screening assays for identifying modulators.
XX
PS Claim 8; Page 104-106; 119pp; English.

The invention relates to isolated human and murine interleukin-9 (IL-9) /IL-2 receptor-like polypeptides. The plasmid containing the encoding cDNA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like polypeptides (16445 proteins) can be recombinantly produced using standard recombinant methodology. The 16445 proteins are used for identifying their modulators and for diagnosis and treatment of immune, inflammatory and respiratory disorders and disorders associated with lungs, colon, kidney and lymphoid tissues including tonsil and thymus, in particular T-lymphocyte-related disorders including atopic conditions such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic inflammatory diseases and graft versus host disease, disorders involving

CC the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney
CC disorders including polyarthritis kidney disease, cystic renal dysplasia,
CC disorders of the thymus including lymphomas, Hodgkin disease and
CC carcinoids. The 16445 polypeptides are also useful as modulating agents
CC in cellular processes including growth promoting activity, particularly
CC the antigen-independent proliferation of T-helper cell clones. The
CC encoding nucleic acid is useful as primers or hybridization probes for
CC the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for
CC tissue typing and in forensic biology. The present sequence represents
CC the human IL-9/IL-2 receptor-like polypeptide (AAB16445)
XX
SQ Sequence 538 AA;
Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 7, 5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGMAAPLLILLLOGGMGCPDLVCTDYLOTVCILMMNLHPSSTLTLTQDQYEBLKD 60
DB 1 MPRGMAAPLLILLLOGGMGCPDLVCTDYLOTVCILMMNLHPSSTLTLTQDQYEBLKD 60
QY 61 EATSCSLHRSANATHTATYTCMDVFFHMDIDIFSUNITDQSGNYSOEGSFLLAESIKP 120
DB 61 EATSCSLHRSANATHTATYTCMDVFFHMDIDIFSUNITDQSGNYSOEGSFLLAESIKP 120
QY 121 APPPNVTVTSGQYNISWRSDYEDPARYMLKGLQYELQYRNRRDPMNVSRRKLISVDS 180
DB 121 APPPNVTVTSGQYNISWRSDYEDPARYMLKGLQYELQYRNRRDPMNVSRRKLISVDS 180
QY 181 RSVSLPLLEPFKDSYELQYRAGPMQSSYOGTSEMSDPVITFOTOSBELKEGNNPHLL 240
DB 181 RSVSLPLLEPFKDSYELQYRAGPMQSSYOGTSEMSDPVITFOTOSBELKEGNNPHLL 240
QY 241 LLLIVIFIPAFMSLKTPLRLMKKIWAAPSPPFFMPLKYGSGDFKKVGAAPFTGSS 300
DB 241 LLLIVIFIPAFMSLKTPLRLMKKIWAAPSPPFFMPLKYGSGDFKKVGAAPFTGSS 300
QY 301 LELGPMSPVSTLEVTSCHPSPSPAKRLQTLTELOEPAELVESDGVKPSWPTAQNNGG 360
DB 301 LELGPMSPVSTLEVTSCHPSPSPAKRLQTLTELOEPAELVESDGVKPSWPTAQNNGG 360
QY 361 SAYSEERDRPYGLVSDIVTVTLDAEGPCTWPCSCEDDGYPALDDAGLESPGLEDPLLD 420
DB 361 SAYSEERDRPYGLVSDIVTVTLDAEGPCTWPCSCEDDGYPALDDAGLESPGLEDPLLD 420
QY 421 AGTTLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTTLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGQAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGQAS 538

RESULT 7
AAB81960
ID AAB81960 standard; protein, 538 AA.
AC AAB81960;
XX AAB81960;
XX 25-NOV-2002 (first entry)
DT Human 16445 protein.
DE Human 16445 protein.
XX Interleukin; IL-9; IL-2; 16445; antiasthmatic; antiallergic; human;
KW antipsoriatic; antiinflammatory; immunosuppressive; cytostatic; virucide;
KW antineumatic; antidiabetic; antidiabetic; antithyroid; dermatological;
KW nephrotropic; antibacterial; tuberculostatic; antileprotic; antipyretic;
KW antitumor; gene therapy; receptor.
XX Homo sapiens.
OS Homo sapiens.
XX US2002090680-A1.
PN

XX	11-JUL-2002.	26-SEP-2001; 2001US-00965313.	99US-00313913.	18-MAY-1999; 2000US-00574100.	(MILL-) MILLENNIUM PHARM INC.	Hodge MR;	WPI: 2002-655832/70.	N-PSDB; ABQ79536.	New interleukin-9/interleukin-2 receptor-like polypeptides and polynucleotides for diagnosing, treating respiratory, T-lymphocyte related disorders and disorders associated with lung, colon, kidney and lymphoid tissues.	Claim 8; Page 31-33; 54pp; English.	The invention relates to isolated interleukin (IL)-9/IL-2 receptor-like polypeptide, 16445. The 16445 polypeptide can be expressed by standard recombinant methodology. The 16445 polypeptide, polynucleotides and their modulators are useful for modulating the immune, inflammatory and respiratory responses, for the diagnosis and treatment of immune and respiratory disorders, particularly for the treatment and diagnosis of T-lymphocyte-related disorders, including, atopic conditions, such as asthma and allergy, including allergic rhinitis, psoriasis, the effects of pathogen infection, chronic inflammatory diseases, organ-specific autoimmunity, graft rejection, and graft versus host disease. The molecules are also useful as modulating agents in a variety of cellular processes including growth promoting activity, particularly the antigen independent proliferation of T helper cell clones, and direct effects on normal haemopoietic progenitors, human T cells, B cells, thymocytes, thymic lymphomas and neuronal cell lines. They are useful for the modulation, diagnosis, and treatment of immune, inflammatory, and respiratory disorders and disorders associated with lungs, colon, kidney, and lymphoid tissues including tonsil and thymus. The present sequence represents a human 16445 polypeptide	Sequence 538 AA;	Query Match Best Local Similarity 100.0%; Score 2958; DB 5; Length 538; Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 MGRMAAPLLLLLLGGWGCPLDVCYTDYLTQVTCILEMNNLHPSTLTWMDQYEELKD 60 1 MBRGMAAPLLLLLLGGWGCPLDVCYTDYLTQVTCILEMNNLHPSTLTWMDQYEELKD 60 61 EATSCSLHRSANNAHTATTCIMDVPHFPAADDIFSVNITDGSNGNSQEGSGFLAESIKP 120 61 EATSCSLHRSANNAHTATTCIMDVPHFPAADDIFSVNITDGSNGNSQEGSGFLAESIKP 120 121 APPPNVTATVFGSGOYNISMRSDYEDPAFYMLKGLQYELQRYRGGPMPAVSPRKLISYDS 180 121 APPPNVTATVFGSGOYNISMRSDYEDPAFYMLKGLQYELQRYRGGPMPAVSPRKLISYDS 180 121 APPPNVTATVFGSGOYNISMRSDYEDPAFYMLKGLQYELQRYRGGPMPAVSPRKLISYDS 180 181 RSVSLPLLEFRKDSSEYELQVRAAGPMPGSSYQGTWSEWSDPVIQTQSEELKEGMNPHLL 240 181 RSVSLPLLEFRKDSSEYELQVRAAGPMPGSSYQGTWSEWSDPVIQTQSEELKEGMNPHLL 240 241 LLLLVIVTFPAWMSLKTPLMLKMKKIYAVSPERPFMPPLLYGCGGDPFRKXVGAFTGSS 300 241 LLLLVIVTFPAWMSLKTPLMLKMKKIYAVSPERPFMPPLLYGCGGDPFRKXVGAFTGSS 300 301 LELGWSPEVPSTLEVYSCHPRPSPAKRLQTLLEQEPALVSDGVKPKSFMTQNSGG 360 301 LELGWSPEVPSTLEVYSCHPRPSPAKRLQTLLEQEPALVSDGVKPKSFMTQNSGG 360 361 SAYSEERDRPYGLVSDITVTYVDADEPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
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[illegible]

CC also be used as nutritional sources or supplements. The present protein sequence represents the human MU-1 haemopoietin receptor superfamily CC chain. MU-1 is also a member of the cytokine receptor family. This CC sequence was used in the invention for the characterisation of previously CC unknown members of the haemopoietin receptor superfamily

XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 5; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLQGGMGCPDLYCYTDYIQYICILEMNNLHPSTLTTLTWODQYEBELKD 60
DB 1 MPRGMAAPLLLLLLQGGMGCPDLYCYTDYIQYICILEMNNLHPSTLTTLTWODQYEBELKD 60
QY 61 EATSCSLHRSANNAHTATYTCMDVFFHMDIFSVNITDQSGNYSGECGFFLAESIKP 120
DB 61 EATSCSLHRSANNAHTATYTCMDVFFHMDIFSVNITDQSGNYSGECGFFLAESIKP 120
QY 121 APPENVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNKGDPAVSPRRKLISVDS 180
DB 121 APPENVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNKGDPAVSPRRKLISVDS 180
QY 181 RSVSLPLLEPRKDSYELQYRAGMPGSSYQGTWSEMSDPYIQTQSEELKEGNNPHLL 240
DB 181 RSVSLPLLEPRKDSYELQYRAGMPGSSYQGTWSEMSDPYIQTQSEELKEGNNPHLL 240
QY 241 LLLLVIFIPAFWGLKTHPLRWKLIWAVSPERFPMPLKGGSGDPKKVAGAPFTGSS 300
DB 241 LLLLVIFIPAFWGLKTHPLRWKLIWAVSPERFPMPLKGGSGDPKKVAGAPFTGSS 300
QY 301 LELGPMSPPEVSTLEVYSCHPPRSPAKRLQTLQEPALVESDQVPKPSFWPTAONSGG 360
DB 301 LELGPMSPPEVSTLEVYSCHPPRSPAKRLQTLQEPALVESDQVPKPSFWPTAONSGG 360
QY 361 SANSEEDRPYGLVITTVYLDKEGCTWPCSCEDGYPALDDAGIEPFGLEDPLD 420
DB 361 SANSEEDRPYGLVITTVYLDKEGCTWPCSCEDGYPALDDAGIEPFGLEDPLD 420
QY 421 AGTTVLSGGCVSAGSPGLGPGLSLDRLKPLPLADGEDMAGGLPMGGSPGCVSESEAGS 480
DB 421 AGTTVLSGGCVSAGSPGLGPGLSLDRLKPLPLADGEDMAGGLPMGGSPGCVSESEAGS 480
QY 481 PLAGLMDTPDPSGCVGSDCSSPVECDFTSPDEBPSPSYLRQWVVIPEPLSSPPGQAS 538
DB 481 PLAGLMDTPDPSGCVGSDCSSPVECDFTSPDEBPSPSYLRQWVVIPEPLSSPPGQAS 538

RESULT 9
AAE13726
ID AAE13726 standard; protein; 538 AA.

XX AAE13726;

XX 26-FEB-2002 (first entry)

XX Human soluble Zalphal1 cytokine receptor protein.

XX Human; Zalphal1; cytokine receptor; immunosuppressive; cytostatic;
XX inflammatory disorder; haemostatic; cell proliferation; immune disorder;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
XX ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
XX viral infection.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19
FT Protein /label= Signal_peptide
FT Protein 20..538
FT Protein /label= Mature_Zalphal1_protein

FT Domain 20..237
FT /label= Cytokine_binding_domain
FT Domain 120..123
FT /label= Domain_linker
FT Region 192..202
FT /note= "penultimate strand region"
FT Domain 214..218
FT /note= "MSXMS motif"
FT Domain 238..255
FT /label= Transmembrane_domain
FT Domain 256..538
FT /label= Intracellular_signalling_domain
FT Region 267..273
FT /note= "Box I signalling site"
FT Region 301..304
FT /note= "Box II signalling site"
FT Binding-site 519..522
FT /label= SPAT3_binding_site

XX W0200177171-A2.

XX 18-OCT-2001.

XX 03-APR-2001; 2001WO-US010872.

XX 05-APR-2000; 2000US-0194731P.

XX 28-JUL-2000; 2000US-0222121P.

XX (ZYMO) ZYMOGENETICS INC.

PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;

XX WPI; 2002-025898/03.

XX N-PSDB; AAD22918.

PT Novel soluble receptor polypeptides and polynucleotides used as cytokine

PT antagonist for stimulating ligand activity-induced proliferation of

PT hematopoietic cells and for suppressing immune response in a mammal.

XX Example 1; Page 172-173; 243pp; English.

CC The invention relates to an isolated soluble zalphal1 cytokine receptor
CC polypeptide and their cDNA molecules. Zalpha proteins are useful for
CC inhibiting or antagonising the ligand activity-induced proliferation of
CC hematopoietic cells and haematopoietic cell progenitors preferably
CC lymphoid cells which are natural killer cells or cytotoxic T cells.
CC Zalpha is useful for treating immune and inflammatory disorders, for
CC reducing proliferation of neoplastic B or T cells, for suppressing an
CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
CC useful for treating diseases that require immune regulation including
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC sepsis, viral infection (dengue virus infection) and cancer. The present
CC sequence is human soluble Zalphal1 cytokine receptor protein

XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 5; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLQGGMGCPDLYCYTDYIQYICILEMNNLHPSTLTTLTWODQYEBELKD 60

DB 1 MPRGMAAPLLLLLLQGGMGCPDLYCYTDYIQYICILEMNNLHPSTLTTLTWODQYEBELKD 60

QY 61 EATSCSLHRSANNAHTATYTCMDVFFHMDIFSVNITDQSGNYSGECGFFLAESIKP 120

DB 61 EATSCSLHRSANNAHTATYTCMDVFFHMDIFSVNITDQSGNYSGECGFFLAESIKP 120

QY 121 APPENVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNKGDPAVSPRRKLISVDS 180

DB 121 APPENVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNKGDPAVSPRRKLISVDS 180

```
QY 181 RSVSLPLPERKDSSEYELQVRAGMPGSSYQGTWSEMSDPIYFOTOSBELKEGNPHLL 240
DB 181 RSVSLPLPERKDSSEYELQVRAGMPGSSYQGTWSEMSDPIYFOTOSBELKEGNPHLL 240
QY 241 LLLLVIFIPAFWMLKTHPLMLMKKIWAVPSEPFEMPLYKCGSGDFKKWVGAPFTGSS 300
DB 241 LLLLVIFIPAFWMLKTHPLMLMKKIWAVPSEPFEMPLYKCGSGDFKKWVGAPFTGSS 300
QY 301 LEIGPMSPEVPSTLEVYSCHPSPRSYAKRLQLTLEQPAELVESGVPKPSFWPTAONSGG 360
DB 301 LEIGPMSPEVPSTLEVYSCHPSPRSYAKRLQLTLEQPAELVESGVPKPSFWPTAONSGG 360
QY 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLD 420
DB 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLD 420
QY 421 AGTTVLSGCVSAGSPGLGSPGLSLDLRLKRPPLADGEDMAGGLPMGGRSPGCVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGSPGLSLDLRLKRPPLADGEDMAGGLPMGGRSPGCVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538

RESULT 10
AAU11978
ID AAU11978 standard; protein; 538 AA.
XX
AC AAU11978;
XX
DT 09-APR-2002 (first entry)
XX
DE Human zai1phal1 receptor polypeptide.
XX
KM CytoKine; zai1phal1 ligand; zai1phal1 receptor; NK cell progenitor;
KM natural killer cell proliferation; T-cell proliferation;
KM B-cell proliferation; anti-tumour response; immune system;
KM immunostimulant; cytoKine; human.
XX
OS Homo sapiens.
XX
PN US6307024-B1.
XX
PD 23-OCT-2001.
XX
PF 09-MAR-2000; 2000US-00522217.
XX
PR 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnson JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI; 2002-040208/05.
DR N-PSDB; AAS20642.
XX
PT New zai1phal1 ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
PS Claim 1; Col 191-194; 105pp; English.
XX
CC The present invention relates to the isolation of a novel cytokine,
CC zai1phal1 ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zai1phal1 receptor and the polynucleotide
CC encoding it. The zai1phal1 ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
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CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
CC zai1phal1 ligand polypeptide is also useful in preparing antibodies that
CC bind to zai1phal1 ligand epitopes. The zai1phal1 ligand polynucleotides can
CC be used as probes or primers to clone regions of a zai1phal1 ligand gene,
CC and in gene therapy. Zai1phal1 ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC human zai1phal1 receptor polypeptide
XX
SQ Sequence 538 AA;
XX
Query Match 100.0%; Score 2958; DB 5; Length 538;
Best Local Similarity 100.0%; Pred. No. 7, 5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLLOGMGCPDLVCTDYLOQYICILEMNNLHPSTLTWTWQDYEBLKD 60
DB 1 MPRGMAAPLLLLLLLOGMGCPDLVCTDYLOQYICILEMNNLHPSTLTWTWQDYEBLKD 60
QY 61 EATSCSIHRSANAHATATYTCHEMDVFHMAADIFSVNITDQSGNYGQECGSFLAASIKP 120
DB 61 EATSCSIHRSANAHATATYTCHEMDVFHMAADIFSVNITDQSGNYGQECGSFLAASIKP 120
QY 121 APPENVTVTFSSGOVNI SWRSVDYEDPAFYMLKGLQYELQVRNKGDDPMVSPRRKLISVDS 180
DB 121 APPENVTVTFSSGOVNI SWRSVDYEDPAFYMLKGLQYELQVRNKGDDPMVSPRRKLISVDS 180
QY 181 RSVSLPLPERKDSSEYELQVRAGMPGSSYQGTWSEMSDPIYFOTOSBELKEGNPHLL 240
DB 181 RSVSLPLPERKDSSEYELQVRAGMPGSSYQGTWSEMSDPIYFOTOSBELKEGNPHLL 240
QY 241 LLLLVIFIPAFWMLKTHPLMLMKKIWAVPSEPFEMPLYKCGSGDFKKWVGAPFTGSS 300
DB 241 LLLLVIFIPAFWMLKTHPLMLMKKIWAVPSEPFEMPLYKCGSGDFKKWVGAPFTGSS 300
QY 301 LEIGPMSPEVPSTLEVYSCHPSPRSYAKRLQLTLEQPAELVESDGYPKPSFWPTAONSGG 360
DB 301 LEIGPMSPEVPSTLEVYSCHPSPRSYAKRLQLTLEQPAELVESDGYPKPSFWPTAONSGG 360
QY 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLD 420
DB 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLD 420
QY 421 AGTTVLSGCVSAGSPGLGSPGLSLDLRLKRPPLADGEDMAGGLPMGGRSPGCVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGSPGLSLDLRLKRPPLADGEDMAGGLPMGGRSPGCVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538

RESULT 11
ABR61402
ID ABR61402 standard; protein; 538 AA.
XX
AC ABR61402;
XX
DT 12-AUG-2003 (first entry)
DE Human IL-21R SEQ ID NO:2.
XX
XX
XX arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
XX immune cell activity; cancer; infectious disorder; antiheumatic;
XX antiarthritic; osteopathic; antipsoriatic; cytosarctic; antibacterial;
XX virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological;
XX neuroprotective; anticancer; antiallergic; antianemic; hepatotropic;
XX antitumor; antiinflammatory; immune response; immune disorder;
XX autoimmune disease; human.
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[illegible]

Qy	181	RSVSLPLPEPKDSSYELQVAGPMPGSSYQGTWSEMGDPVIFQOSEELKKGMPHLIL	240
I ¹	181	RSVSLPLPEPKDSSYELQVAGPMPGSSYQGTWSEMGDPVIFQOSEELKKGMPHLIL	240
Db	181	RSVSLPLPEPKDSSYELQVAGPMPGSSYQGTWSEMGDPVIFQOSEELKKGMPHLIL	240
Qy	241	LLLLIVIEPAFAWSLKTPLRLMLWKIWAVPSPERFEMPLYKGCSDGFEKMGAPFTGSS	300
Db	241	LLLLIVIEPAFAWSLKTPLRLMLWKIWAVPSPERFEMPLYKGCSDGFEKMGAPFTGSS	300
Qy	301	LELGPMSSEVSTLEVYSCHPRRSPAKLQLTLEQPAELVESDVPKPSFMPATONSGG	360
Db	301	LELGPMSSEVSTLEVYSCHPRRSPAKLQLTLEQPAELVESDVPKPSFMPATONSGG	360
Qy	361	SAYSEBRRPYGLVSDITVTYLDABGCTWPCSCCEDDQYPALDLDAGLESPGLDPLLD	420
Db	361	SAYSEBRRPYGLVSDITVTYLDABGCTWPCSCCEDDQYPALDLDAGLESPGLDPLLD	420
Qy	421	AGTTVLSGCVSAGSPGLGPGILDLRLKPLADGEDWAGLPGNGRSPGVSESEAGS	480
Db	421	AGTTVLSGCVSAGSPGLGPGILDLRLKPLADGEDWAGLPGNGRSPGVSESEAGS	480
Qy	481	PLAGLMDTFRSGSPGSSPVEDFTFSPDEGPPRYLRQWVYIIPPLSSPGPAS	538
Db	481	PLAGLMDTFRSGSPGSSPVEDFTFSPDEGPPRYLRQWVYIIPPLSSPGPAS	538

RESULT 12

AAE14939

ID AAE14939 standard; protein; 538 AA.

XX AAE14939;

XX 27-AUG-2003 (first entry)

DT Human interleukin-21 (IL-21) receptor.

XX Interleukin-21; antagonist; cancer; inflammatory; autoimmune disorder;

KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;

KW myasthenia gravis; diabetes; human; zalphal receptor; IL-21 receptor.

XX Homo sapiens.

OS WO2003040313-A2.

PN 15-MAY-2003.

PD 28-OCT-2002; 2002WO-US034502.

PF 05-NOV-2001; 2001US-0337586P.

XX (ZYMO) ZYMOGENETICS INC.

PA Presnell SR, West JW, Novak JE;

XX WPI; 2003-441547/41.

DR N-PSDB; AAD47859.

XX New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing

PT and treating disorders with aberrant expression or activity of the IL-21

PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and

PT diabetes.

CC Example 1; Page 65-67; 71pp; English.

CC myasthenia gravis and diabetes. The polypeptides can also be used to
CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
CC and for enhancing in vivo killing of target tissues. The present sequence
CC is human IL-21 receptor (originally designated zalpahal receptor)
XX
XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYIQTVICILEMNNLHPSTLTTLTWODQYEBELKD 60
DB 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYIQTVICILEMNNLHPSTLTTLTWODQYEBELKD 60
QY 61 EATSCSLHRSANAHATATYTCMDVFFHMDIFSVNITDQSGNYSQEGCSFLLAESIKP 120
DB 61 EATSCSLHRSANAHATATYTCMDVFFHMDIFSVNITDQSGNYSQEGCSFLLAESIKP 120
QY 121 APPFNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMAVSPRRKLISVDS 180
DB 121 APPFNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMAVSPRRKLISVDS 180
QY 181 RSVSLPLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
DB 181 RSVSLPLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
QY 241 LLLIVYFIAPFWSLKTNPRLMKKIWAIVSPERFPMPLKYKCGSGDFKMWGAPFTGSS 300
DB 241 LLLIVYFIAPFWSLKTNPRLMKKIWAIVSPERFPMPLKYKCGSGDFKMWGAPFTGSS 300
QY 301 LELGPMSPVSTLEVYSCHPPRSAPAKRLQTLQEPALVELVESGVPKSPWPTAQNSSGG 360
DB 301 LELGPMSPVSTLEVYSCHPPRSAPAKRLQTLQEPALVELVESGVPKSPWPTAQNSSGG 360
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLIEDPLLD 420
DB 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLIEDPLLD 420
QY 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTFTDGSFVSGDSSPVCECDFTSPGDEGPPRSYLQWVVIIPPLSSPGQAS 538
DB 481 PLAGLMDTFTDGSFVSGDSSPVCECDFTSPGDEGPPRSYLQWVVIIPPLSSPGQAS 538

RESULT 13
ABU62888
ID ABU62888 standard; proteoin; 538 AA.

XX AC ABU62888;
XX DT 15-SEP-2003 (first entry)
XX DE Human MU-1 haematopoietic receptor superfamily chain.
XX KM Human; MU-1; haematopoietic receptor superfamily chain; immunomodulator;
XX KM cytoactive; antibacterial; virucide; antianaemic; gene therapy;
XX KM haematopoietic; anaemias; immune response; cancer; infection;
XX KM transplanted organ; cytokine; receptor.
XX OS Homo sapiens.
XX PN US2003049798-A1.
XX PD 13-MAR-2003.
XX PF 04-OCT-2001; 2001US-00972218.
XX PR 17-MAR-1998; 98US-00040005.
XX PR 26-APR-2000; 2000US-00560766.

PR 11-MAY-2000; 2000US-00569384.

XX (CART/) CARTER L.
PA (WHIT/) WHITTERS M J.
PA (COLL/) COLLINS M.
PA (YOUN/) YOUNG D A.
PA (DONA/) DONALDSON D D.
PA (LOWE/) LOWE L D.
PA (UNGE/) UNGER M.

XX Carter L, Whitters MJ, Collins M, Young DA, Donaldson DD;
PI Lowe LD, Unger M;
XX WPI: 2003-512354/48.
DR N-PSDB: ACD26717.

XX New fusion polypeptide for regulating hematopoiesis and immune responses,
PT comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion
PT polypeptide.

XX Claim 13; Fig 4; 26pp; English.

XX The invention describes a fusion polypeptide comprising at least a
CC fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide. The
CC polypeptide is useful in regulating haematopoiesis (e.g. in cases of
CC anaemias) and/or immune responses (e.g. immune response to cancer,
CC infections or to a transplanted organ) and in identifying other members
CC of the haematopoietic superfamily, including cytokines and receptors. The
CC polypeptide may be used to express recombinant protein for analysis,
CC characterisation or therapeutic use; and as markers for tissues or
CC chromosomes. The polypeptide and polynucleotide may also be used as
CC nutritional sources or supplements. This is the amino acid sequence of
CC human MU-1 haematopoietic receptor superfamily chain

XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYIQTVICILEMNNLHPSTLTTLTWODQYEBELKD 60
DB 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYIQTVICILEMNNLHPSTLTTLTWODQYEBELKD 60
QY 61 EATSCSLHRSANAHATATYTCMDVFFHMDIFSVNITDQSGNYSQEGCSFLLAESIKP 120
DB 61 EATSCSLHRSANAHATATYTCMDVFFHMDIFSVNITDQSGNYSQEGCSFLLAESIKP 120
QY 121 APPFNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMAVSPRRKLISVDS 180
DB 121 APPFNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMAVSPRRKLISVDS 180
QY 181 RSVSLPLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
DB 181 RSVSLPLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
QY 241 LLLIVYFIAPFWSLKTNPRLMKKIWAIVSPERFPMPLKYKCGSGDFKMWGAPFTGSS 300
DB 241 LLLIVYFIAPFWSLKTNPRLMKKIWAIVSPERFPMPLKYKCGSGDFKMWGAPFTGSS 300
QY 301 LELGPMSPVSTLEVYSCHPPRSAPAKRLQTLQEPALVELVESGVPKSPWPTAQNSSGG 360
DB 301 LELGPMSPVSTLEVYSCHPPRSAPAKRLQTLQEPALVELVESGVPKSPWPTAQNSSGG 360
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLIEDPLLD 420
DB 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLIEDPLLD 420
QY 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTFTDGSFVSGDSSPVCECDFTSPGDEGPPRSYLQWVVIIPPLSSPGQAS 538

Db 481 PLAGLMDTDFSGVSDCCSPVECDFTSPQDEGPPRSYLQWVVIPEPLSSPPQAS 538
RESULT 14
ABW00881
ID ABW00881 standard; protein; 538 AA.
AC ABW00881;
XX 15-JAN-2004 (first entry)
XX Human cytokine receptor, zalphall protein.
XX
XX Cytokine receptor; zalphall; cell proliferation; cell development;
XX spleenic disorder; blood disorder; bone disorder; immune disorder;
XX haematopoietic; lymphoid; inflammatory; therapy; receptor; human.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX /label= Signal_peptide
XX Protein 20..538
XX /note= "Mature human zalphall protein"
XX Binding-site 20..237
XX /note= "Cytokine-binding domain"
XX Region 120..123
XX /note= "Domain linker"
XX Region 192..202
XX /note= "Penultimate strand region"
XX Domain 214..218
XX /note= "WSXWS motif"
XX Domain 238..255
XX /note= "Transmembrane domain"
XX Domain 256..538
XX /note= "Intracellular signalling domain"
XX Region 267..273
XX /note= "Box I signalling site"
XX Region 301..304
XX /note= "Box II signalling site"
XX
XX US6576744-B1.
XX
XX 10-JUN-2003.
XX
XX 23-SEP-1999; 99US-00404641.
XX
XX 23-SEP-1998; 98US-0100896P.
XX 09-MAR-1999; 99US-0123546P.
XX 06-JUL-1999; 99US-0142574P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;
XX WPI; 2003-799829/75.
XX DR N-PSDB; AAD61882.
XX
XX Novel cytokine receptor zalphall useful for treating lymphoid, immune,
XX inflammatory, spleenic, blood or bone disorders.
XX
XX Claim 1; Fig 2; Opp; English.
XX
XX The invention relates to a cytokine receptor designated zalphall and its
XX nucleic acid sequence. Zalphall protein is useful for detecting ligands
XX that stimulate the proliferation and/or development of haematopoietic,
XX lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful
XX in identifying a region of the genome associated with human disease
XX states. Zalphall protein is useful for treating lymphoid, immune,
XX inflammatory, spleenic, blood or bone disorders. The present sequence is
XX human Zalphall protein

SQ Sequence 538 AA:
Query Match 100.0%; Score 2958; DB 7; Length 538;
Best Local Similarity 100.0%; Pred. No. 7, 5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGMAAPLLLLLLQGGMGCPDLYCYTDYLTQTVICILEMNNLHPSTLTLTQDDQYEEELKD 60
DB 1 MPRGMAAPLLLLLLQGGMGCPDLYCYTDYLTQTVICILEMNNLHPSTLTLTQDDQYEEELKD 60
QY 61 EATSCSLHRSAHNATHATYTCMDVFFHMAADIFSVNITDQSGNYSQEGSFLAESIKP 120
DB 61 EATSCSLHRSAHNATHATYTCMDVFFHMAADIFSVNITDQSGNYSQEGSFLAESIKP 120
QY 121 APPPNVTVTSGQYNISRSDDYEDPAFYMLKGLQYELQYRNKCDPMAVSPRRKLISVDS 180
DB 121 APPPNVTVTSGQYNISRSDDYEDPAFYMLKGLQYELQYRNKCDPMAVSPRRKLISVDS 180
QY 181 RSVSLLEPRKDSYSYLOVRAGPMGSSYQGTWSEMSDPVIFOTOSBELKEGNNPHLL 240
DB 181 RSVSLLEPRKDSYSYLOVRAGPMGSSYQGTWSEMSDPVIFOTOSBELKEGNNPHLL 240
QY 241 LLLLVIFIPAFMSLKTHPMLRLMKKIWAAPSRRFFMPLYKSGSDPKKVVGAPEFTGSS 300
DB 241 LLLLVIFIPAFMSLKTHPMLRLMKKIWAAPSRRFFMPLYKSGSDPKKVVGAPEFTGSS 300
QY 301 LEIGPMSPVEPSTLEVYSCHPSPSPAKRLQTLTEQEPALVESDGVKPSFWPTAONSGG 360
DB 301 LEIGPMSPVEPSTLEVYSCHPSPSPAKRLQTLTEQEPALVESDGVKPSFWPTAONSGG 360
QY 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSEDDGYPLADAGLBPSPGLDEPLLD 420
DB 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSEDDGYPLADAGLBPSPGLDEPLLD 420
QY 421 AGTVLSCGCVSAGSPGLGSPGLSLDLRLKPLADGCDMAAGLPMGGRSPGVSESEAGS 480
DB 421 AGTVLSCGCVSAGSPGLGSPGLSLDLRLKPLADGCDMAAGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFSGVSDCCSPVECDFTSPQDEGPPRSYLQWVVIPEPLSSPPQAS 538
DB 481 PLAGLMDTDFSGVSDCCSPVECDFTSPQDEGPPRSYLQWVVIPEPLSSPPQAS 538
RESULT 15
ADG87460
ID ADG87460 standard; protein; 538 AA.
XX
XX ADG87460;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human zalphall protein.
XX
XX zalphall; anaemia; human; gene therapy.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX /label= Signal_peptide
XX Protein 20..538
XX /note= "Human mature zalphall protein"
XX Domain 20..237
XX /note= Cytokine binding domain
XX Region 120..123
XX /note= "Domain linker"
XX Region 192..202
XX /note= "Penultimate strand region"
XX Domain 238..255
XX /note= Transmembrane domain
XX Domain 256..538
XX /note= Complete intracellular signalling domain
XX Region 267..273

FT /note= "Box I signaling site"
FT Region 301..304
FT /note= "Box II signaling site"

US2003148447-A1.

07-AUG-2003.

13-SEP-2002; 2002US-00243072.

28-JUL-2000; 2000US-00628127.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Conklin DC, Novak JE, Hammond AK;

WPI; 2003-897570/82.

N-PSDB; ADG87459.

XX New polynucleotide, useful for preparing a composition for treating e.g.,
PT anemia encodes a zalphall polypeptide cytokine receptor.

PS Claim 1; SEQ ID NO 2; 91pp; English.

CC The present invention relates to new isolated polynucleotide encoding
CC zalphall polypeptide. The polynucleotide is useful for treating anaemia.
CC The invention is useful for producing zalphall polypeptide and producing
CC an antibody to zalphall polypeptide. The present sequence is human
CC zalphall protein.

XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;

Best Local Similarity 100.0%; Pred. No. 7.5e-240; Mismatches 0; Indels 0; Gaps 0;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLOGGMGCPDLVCYTDYLTQVLCILEMNLHPSTLTLTWQDYBELKD 60

Db 1 MPRGMAAPLLLLLOGGMGCPDLVCYTDYLTQVLCILEMNLHPSTLTLTWQDYBELKD 60

QY 61 EATSCSLHRSANHTAHTTTCMDVPHFMADDFSVNITDQSGNYSQECGSFLLAESIKP 120

Db 61 EATSCSLHRSANHTAHTTTCMDVPHFMADDFSVNITDQSGNYSQECGSFLLAESIKP 120

QY 121 APPENNVVTSGQYNIISMRSDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRKLISVDS 180

Db 121 APPENNVVTSGQYNIISMRSDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRKLISVDS 180

QY 181 RSVSLPLEFRKDSYELQVRAGPMGSSYQGTSEMSDPVIFOTOSSELKEGNNPHLL 240

Db 181 RSVSLPLEFRKDSYELQVRAGPMGSSYQGTSEMSDPVIFOTOSSELKEGNNPHLL 240

QY 241 LLLIVIVIFPAFWSLKTHTPLRLWKKIWAVSPERFEMPLYKCGSGDFKKVVGAPFTGSS 300

Db 241 LLLIVIVIFPAFWSLKTHTPLRLWKKIWAVSPERFEMPLYKCGSGDFKKVVGAPFTGSS 300

QY 301 LELGPMSPPEVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVPRKPSFTPAQNSGG 360

Db 301 LELGPMSPPEVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVPRKPSFTPAQNSGG 360

QY 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCEDDGPALDLADGLESPGLEDPILD 420

Db 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCEDDGPALDLADGLESPGLEDPILD 420

QY 421 AGTTVLSGCGVSAGSPGLGRLGLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480

Db 421 AGTTVLSGCGVSAGSPGLGRLGLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480

QY 481 PLAGLMDTPTDSGVSFVGSPPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPOAS 538

Db 481 PLAGLMDTPTDSGVSFVGSPPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPOAS 538

Search completed: September 7, 2006, 12:44:55
Job time : 226.866 secs

QY 327 RRLQLTELGEPAELVESGVPKPSFMTAKNSGASVAEERDRPGLVISITVTVLADAG 386
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 329 ERDKVTQL-----LQQQKVPEPA---SLSSNHSLTCTFTNOGYFFPHLPDALEIEA- -- 377
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 387 PC-----TWPCSEDD-----GYPALDLDAGLEPSPGLEDDLDTGVTLSCGCVSASAP 436
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 378 -CQVFYTDYPDYSEEDPDGCVAGALPTGSSPOLQLPGS-ED---DAYCTFPSSRDULLFSR 432
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 437 G-LGGP-----LGSLDLRKPLPAD--GEDAGGLPWGGRSPG 471
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 433 SLGGSPSPSTAFPGSGAGGERMMPSLQERVRPRDM-DQPLGAPPFG 478
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 2

interleukin 2 receptor beta chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
C:Accession: B46535
R:Page, T.H.; Dailman, M.J.
Eur. J. Immunol. 21, 2133-2138, 1991
A:Title: Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha and beta chains
A:Reference number: A46535; MUID:91364784; PMID:1889461
A:Accession: B46535
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-537 <PAG>
A:Cross-references: UNIPARC:UPI000017987A
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBI:60818, NCBI:60819)
C:Superfamily: interleukin-2 receptor beta chain, fibronectin type III repeat homology
C:Keywords: cytokine receptor

Query Match	8.4%;	Score 249;	DB 2;	Length 537;
Best Local Similarity	23.5%;	Pred. No. 4.2e-10;		
Matches 148;	Conservative 70;	Mismatches 177;	Indels 234;	Gaps 34

```

QY      5 WAAPL--L L L L L O G W-----G C P D V C Y D Y L Q T V I C I E M M N L H P S T L T L W D O Y E      56
Db      8 W R L P L Y I L L L L L A T T W S A A V N D C S H L K C F Y N S R A N V S C--M M S-----49
QY      57 E L K D E A--T S C S L H R S A H-----N A T-----H A T Y C H M-----D V H F M A D D I F S V      96
Db      50 --P E E A L N V T S C H I H A S D M R H M N K T C E L T P V R Q A S M A C N I L G P L P D S O L T S V D L S T      107
QY      97 N I T--D O S G N S O E C G S F L I A E S I K P A P F V N V T F--S G O Y I S M R-----S D Y E D P A F Y      148
Db      108 S V C W E E E G M R R V T C N H P F D N I R L I A P H S L Q U L H I T R C N I S M E V S Q V S H Y N P---164
QY      149 M L K G L O Y E L O Y R N R G D P W A V S P R K L I S V D S R S V S L L P F E R K-----D S S Y E L      198
Db      165 ----Y L E P E-----A R R L L D R S M E D A S V S L K O R Q O W I F L E T L P D T S Y E L      207
QY      199 Q V R A G P M P G S S Y O G T W S E M S D P V I F O T O S E L K E G M N H L L L L L V I V F I P A W S-----254
Db      208 Q V R V I A O R G K T--R T W S P W S Q P M A F R T R P A D P K E I F P L P M W R C L L V Y G C F F G L S C Y C V      265
QY      255 -----L K T H P L M R L M W K I W A V S P E R F E M P L K G S G D P K K W G A P F-----296
Db      266 L V K R R Y I G P M L K T L L K C H-----I P D P S E F S Q L S S O H G G D L Q K W L S G V P O S F      314
QY      297 ---T G S S L E L G P M S P E V S T L E V Y S C H P P R A S P A K R L Q T L E Q E P A E L V E S G V P K S P F W P      353
Db      315 F S P I G S A P E I S P-----L E V I D-----R D S K T M Q U L L R Q K-----E K A S S P S P S---353
QY      354 T A O N S G G A S E E R D R P Y G L V S I D T V T V L D A E G P C T W---P C---S C E D D G Y P A L D I D A      406
Db      354 --G H S O A S C F T N Q-----G Y F F H L S N A L E I E S C O V Y P Y P C M E D V E E D G--P R L P E E S      405
QY      407 G L E P-----S P G L E D P L L D A G T V L S C G C V S A S P G L G P L-----G S L D R L      449
Db      406 P L P R L L P F T G E Q D D Y C A F P P R D D L L-----F S P I S T N T A V G N S I T P E E      451

```

Dy
KPLRLAGEWMAGLPGGGRSGGVSEESAGSPPLAGLMDITDFDSGFVSDCSSPVECPFTS 509

Dd
RPLSLIQE-----GLP-----SLASDILNGL-----QHLEIEL-- 480

Dy
PDDEGPPRSYLROWVVIPPLSSPPQNAS 538

Dd
GDDEGMS-----TNSSSQQNAS 497

RESULT 3

interleukin-2 receptor beta chain precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 27-Jul-1990 #sequence revision 27-Jul-1990 #ext_change 09-Jul-2004
C.Accession: A35052
R.Kono, T.; Doi, T.; Yamada, G.; Hatakeyama, M.; Minamoto, S.; Tsudo, M.; Miyasaka, M.; Iwano, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 1806-1810, 1990
A.Title: Murine interleukin-2 receptor beta chain: dysregulated gene expression in lymphoma
A.Reference number: A35052; MUID:90175385; PMID:2155425
A.Accession: A35052
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-539 <KON>
A.Cross-references: UNIPROT:P16297; UNIPARC:UPI00000003F82; GB:M28052; NID:G19813; PIDN:
C.Superfamily: Interleukin-2 receptor beta chain; Fibronectin type III repeat homology
Keywords: cytokine receptor; transmembrane protein

Query Match	Score	DB 2	Length
8.4%	247.5	539	

Matches 138; Conservative 68; Mismatches 198; Indels 179; Gaps 29;

QY 5 WAPL--LLLLLGGW-----GCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYE 5

Db 8 WSLSLYVFLLLATPWASAAVKNCSHLECFYNSRANVSC---MWS-HEEALNV-----5

57 EKDEATSCSLHRSAHNATHATYTCHMDVFH-----FMADDIFSVNI 9

Db 57 -----TTCHVHAKS-NLRHWNKTCELTIVRQASWACNLLIGSFPEQSLSVDLBDIN 1

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99 T--DQSGNYSQECGSFLLAESIKPAPFNVIVIF--SGQYNISWR---SDIEDPAFIML
QY

```

DB 110 VCWEEKGWRVKICDFHPFDNLRVAFHSBQVNHIDIQKCNISMKVSQVSHIIEF-----

151 AGNTQIEBQIKNKQDFWAVSFKNNWISVDKSVQBUFEFKNDSSIEBQVNAQVETFEQOOI 2

[illegible][illegible][illegible]

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

[illegible]

SECRET
----- WPCCFDDCY - - - PA 4

369 EEEET DNAT ETESCOVYFTYDPCVEFEVEFEDGSPV.PEGSRYRPL.T.PI.AGEODNYCAEPBR 4

402 T.DI.DAGI.EPSPGI.EDPI.T.DAGTT-----VLSCGCVSAGSPGIGGPLGSLLDRLKPP 4

428 DDL---LLESPSLSTPNTAYGGSRAPERSPLSLHEGLPSLASRDLMG-LORPLERM--P 4

453 LADGEDWAGGLPWGGRSPGCVSESEAGSP-----LAGLDM 488

Db 482 EGDGE-----GLSANSSEGEQASVPEGNLHGQDD 510

RESULT 4

A35782
Cytokine receptor common beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
R:Accession: A35782
R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreure, J.; Yonehara, S.; Yahara, I.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protei
A:Reference number: A35782; MUID:90319131; PMID:1695379
A:Accession: A35782
A:Molecule type: mRNA
A:Residues: 1-896 <GOR>
A:Cross-references: UNIPROT:P26955; UNIPARC:UPI000002785; GB:M34397; NID:9191821; PIDN:
C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 recept
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor
C:Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-896/Product: cytokine receptor common beta chain #status predicted <EXT>
F:23-441/Domain: extracellular #status predicted <EXT>
F:23-235/Domain: cytokine receptor homology <CRS1>
F:253-434/Domain: cytokine receptor homology <CRS2>
F:442-463/Domain: transmembrane #status predicted <TM>
F:464-896/Domain: intracellular #status predicted <INT>

Query Match 7.9%; Score 233; DB 1; Length 896;
Best Local Similarity 20.4%; Pred. No. 1.1e-08;
Matches 113; Conservative 86; Mismatches 220; Indels 134; Gaps 23;

Qy 22 DLVCTYLQTVLCILEMWN-----LHPTLTLTWQDYBELKDEATCSLHRS 70
Db 250 NLQGFPGIGISLHSMWEWTTGTSVSGCLFYRSPVA-----PEEKCPYVKEP 299
Qy 71 AHNATHATYTCMDVFFHMADDFISVNTDGSNGVSGCSFLLA-ESIKAPP-FNVTV 128
Db 300 PGASVYTRYHSLVPEPSAHSQYTVSK-----HLEQGFIMSYNHIQMEPTLNLTK 353
Qy 129 TFSQGVNISMRSQVDEDPAYMLKGLQYELQYRNKGPWMAVSPRKISVDSRSVSLPL 188
Db 354 N-RDSTYLMHETQMAVSFT---EHTFOVQYKKKSDSMDSKTENLDRAHSMDS---- 404
Qy 189 EFRKDSYELQVRAPMGSGSYQGTWSEWSDPVI.FOTQSEBELKEGWNPHLLLVIV 248
Db 405 QLEBDTSCARVAKPT--SNYDGIWMSKSEETWMT-DWMPPLMIVLILVFLITLTL 461
Qy 249 IPAFWSLKTHPLMLMKIWAVPSPERFMPLYKCGSDGFKKWWGAPRTGSSLELWSP 308
Db 462 ILRGCVSVRYTKMKKE--KIPNPSKSL-----FQDGGKGLMP--- 499
Qy 309 EVPSTLEVYSCHRP--RSPAKRLQTLQEPALVELVSDGVKPSFWPTAQNSSGSAVSEE 366
Db 500 --PGSMAAFATKNALQOPQSR-LAEQ-----GESYVHL 532
Qy 367 RDRPYGLVSDITVVL--DAEGPCTWPCSCD--DGYPALDLDALEBPSGLIEDPLDAG 422
Db 533 EDNNVSPLETDPIIIRVPSGPDTPAASESTEQLRPNVYEGPTPRKPKQLSPED-- 590
Qy 423 TTVLSGCVSAKSPGLGP---LGSLLDLRLKPLADGE---DWAGGLPMWGRSPG-- 472
Db 591 -----FNGPYLGPQGHSLPDLQSGPQVGGSLKRALPGSLRYWCLAPGGQVQ 640
Qy 473 -----VSESEASPLAGLDMOTFDGFGVSDCSSPPECFTSPGDEGPRRSYLKQNV 525
Db 641 LVPLSQVMGQOQANDVOCGSSLETSGSPSVKPNPVELSMEOEARNDP----- 691
Qy 526 IPPPLSSGPGQAS 538
Db 692 VTLPISSGSGPBG 704

RESULT 5
A45268
interleukin-9 receptor precursor - mouse
C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
R:Accession: A45268
R:Renauld, J.C.; Druetz, C.; Ketmonni, A.; Housseau, F.; Uytendhove, C.; Van Roost, E.; V
Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992
A:Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs.
A:Reference number: A45268; MUID:92302307; PMID:1376929
A:Accession: A45268
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-468 <REN>
A:Cross-references: UNIPROT:Q01114; UNIPARC:UPI000000057; GB:M4746; NID:9194044; PIDN:
A:Note: authors translated the codon GGG for residue 394 as Glu
C:Keywords: glycoprotein, receptor, T-cell proliferation, transmembrane protein

Query Match 7.5%; Score 221.5; DB 2; Length 468;
Best Local Similarity 23.2%; Pred. No. 3.3e-08;
Matches 134; Conservative 60; Mismatches 181; Indels 203; Gaps 34;

Qy 3 RGNAPPLLLLLLOGWG--CPDLVCTYDYLQTVLCILEMWNLHPTLTL-----TW----- 51
Db 36 RGVSV-----EQGGGQKAGAFCLSNSTYRDC-----HNSABELQESNALLFT 83
Qy 52 QDYELKDEAT-----SCSLHRSANNA-----THATYTCMDVFFHMADDFISVNTDQSG 103
Db 84 SNQVTEIKHKCTFWDNSCTLVLPKEEVFLPNDFTILHRCI---MGQE--QVSLVD--- 135
Qy 104 NYSQCCSFLAELSIKAPPNNV-TVTFSGQVNISSMSQVDEDPAYMLKGLQYELQYRN 162
Db 136 -----SQYLPRRHIKIDPSPDLQSNVSSGCVLTWGINL--ALEPLITLSYELAFKR 186
Qy 163 RGDPMVAVSPRKILSVDSRSVSLPL.EFRKDSYELQVRA-----GPMGSSSYQGTW 214
Db 187 QEEWENRKHDRIVGV--TWLILEAVLNPGSIYEAALRVQMTLESYEDKTEGTYKSHW 244
Qy 215 SEMSDPVI.FOTOSBELKEG-----WNPHLLLLLVIVIFAPFWSLK--THPLML-- 263
Db 245 SEMGQPSF--PSQRRQGLLVPRWQMSASIL-----VVVPIFLLTGFWHLFLKSP 295
Qy 264 -WKIM--AVSPERFMPLYKCGSDGFKKVVGA.PFGSSILELQPMSPVEVSTLEVYSCH 320
Db 296 RLKRI.FQNIIPSPAPFPHPLVSYVHGDFQSGTGRAG----- 333
Qy 321 PPRSPAKRLQTLQEPALVELVSDGVKPSFWPTAQNSSGSAVSEE 376
Db 334 -----PARKNGVSTSGSBS-----SIW 353
Qy 377 DTVTVLDAEGPCTWPCSC-----EDDGYPALDLDALEBPSGLIEDPLDAGTVLSCGV 431
Db 354 EAVATILTYSPACVQFACLKMEATAPGFGI-----PGSEH-----VLPAGCL 396
Qy 432 S-AGSPGLGRLGSLDLRLKPLADGEDWAGLFWGRSPGVSEASGAPLAGLDMDTF 490
Db 397 ELBQPSAVLP-----QEDWA---PLGSARP--PPDSDSGS----- 428
Qy 491 DSGFVSDCSSPVGCDFTS--PGDEGPRRSYLKQNV 527
Db 429 -SDYCMLDCE--ECHLSAPFGHTESPCLTLAGVAPL 463

RESULT 6
A40091
interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
R:Accession: A40091; A43022
R:Itoh, N.; Yonehara, S.; Schreure, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara, I
Science 247, 324-327, 1990
A:Title: Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene
A:Reference number: A40091; MUID:90117145; PMID:2404337
A:Accession: A40091
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-878 <ITO>

A/Cross-references: UNIPROT:P26954; UNIPARC:UPI000015742D
R:Gorman, D.M.
Submitted to Genbank, November 1989
A/Reference number: A43022
A/Accession: A43022
A/Molecule type: mRNA
A/Residues: 1-815, 'O', 817-878 <GOR>
A/Cross-references: UNIPARC:UPI000020F033; GB:M29855; NID:G198342; PIDN:AA39295.1; PID:
C/Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains a
receptor.
C/Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h
C/Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-878/Product: interleukin-3 receptor beta chain #status predicted <EXT>
F:23-440/Domain: extracellular #status predicted <EXT>
F:33-233/Domain: cytokine receptor homology <CRS1>
F:254-433/Domain: cytokine receptor homology <CRS2>
F:441-462/Domain: transmembrane #status predicted <TM>
F:463-878/Domain: intracellular #status predicted <INT>

Query Match 7.4%; Score 218.5; DB 1; Length 878;
Best Local Similarity 21.5%; Pred. No. 1.2e-07;
Matches 119; Conservative 79; Mismatches 219; Indels 137; Gaps 25;

OY 22 DLVCTVTLQTVICILEMNLHPSTLTLMQDYELKDEATSCSLHRSANHTATYTC 81
DB 251 NLQGFPGICGLHSCWEWTTGTSRGLEFRRSPAPREKCSPTVVEPQASVYTRRC 310
OY 82 HMDVFHFMADDIFSVNITDQSGNYSQECGFLLA-ESIKPAPFNVTATSGQYNISMS 140
DB 311 SLRPPESASAHQYTVSVK-----HLEQGFIMSYVHQMPPILNQTKNDSYSLHET 364
OY 141 D-----YDDPARYMLKGLQYELQYRNKRDPMWAVSPRKLISVDSRSVLLPLERKSSY 196
DB 365 QKIPKYIDHTF-----QVYKKKSSKSKDKTENTGRVNSMD--LF-QLEPDTSY 411
OY 197 ELQVRAQPMPSYQGTWSEWDVIFQTOSEELKEGW-NPHLLLLLLLVIVFIIPA----- 251
DB 412 CARRVKPI--SDVDGIMSEWSNEYWTID-----WVMTLWIVLIVLITLITLLAL 462
OY 252 -FWSLKTPLRLMKKIWAIVSPERFEMPLKYGCGSGDFKVVAGAPFTGSSLELGPWSDEV 310
DB 463 HFGVYVGYRTYRKWKE--KIPNPSKSLT-----FQDGGKLMF----- 498
OY 311 PSTLEVVSCHRP--RSPAKRLQLTLEQ-----EPALVESGVKPKSPFWPTAQ 356
DB 499 PGSMVAAPATKXNPALQGPQSR-LAEQGVSYEHLNENNSPLTIEDPIIDP--BSRP 554
OY 357 NSGSAVSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALESPGLE 416
DB 555 DTPPAASE-----STEQLEPNVQVEGPI--PSSRPKQLPSFDN-----GPYIGP 598
OY 417 PLLDAGTTVLSGCVSAGSPGLGSPGLG--LLDLKPLADGEDWAGGLPMGSGSPG-- 472
DB 599 P-----QSHSLPDLPGQLGSPQVGSGLKFPAL-----PGSLFYMCLPFGQV 639
OY 473 -----VSESEAGSPLAGLMDPTFDSGFVSGSCSSVECDFTSPDEGEPRTYLNQW 524
DB 640 QLVPLSQVMGGQMDVQCGSSLTGTGSPVPEKPNPELVSEKQEARDNPMTL----- 694
OY 525 VIPLPLSPGPQAS 538
DB 695 -----PISSGPEGS 704

RESULT 7

B45268
interleukin-9 receptor precursor - human
C/Species: Homo sapiens (man)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C/Accession: B45268
R:Renauld, J.C.; Druetz, C.; Kermouni, A.; Housseau, F.; Uytendhoe, C.; Van Roost, E.; V
Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992

A/Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs.
A/Reference number: A45268; MUID:92302307; PMID:1376929
A/Accession: B45268
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-522 <REN>
A/Cross-references: UNIPROT:Q01113; UNIPARC:UPI000016AAD3; GB:M64747; NID:G184508; PIDN:
C/Keywords: glycoprotein; receptor; T-cell proliferation; transmembrane protein

Query Match 7.3%; Score 215; DB 2; Length 522;
Best Local Similarity 24.9%; Pred. No. 1.1e-07;
Matches 137; Conservative 52; Mismatches 200; Indels 162; Gaps 33;

OY 35 CILEMNLHPSTLTLMQDYELKDEATSC-----SLHRSANHTATYTC 80
DB 6 CIMEGMLTLEBALRDMGTW-----LLACICTCTVCGLGVSTGCGGRSTFT 55
OY 81 C-----HMDVFHFMADD-----IFSVNITDQSGNYSQECGFLLAESIKP 120
DB 56 CLTNMILRIDC-HMSAPDELQGGSSPMLLFTSN-QAPGTHKCLIRGSECTVLPPEAVL- 112
OY 121 APPENVTVTF--SGQYNISW-----RSDE-----DPAF 147
DB 113 VPSDNFTITPHHCHMSGREQVSLVDPEYLPRRHVCLDPPSLQSNISSGHCILTWSISPAL 172
OY 148 YMLKGLQYELQYRNKRDPMWAVSPRKLISVDSRSVLLPLR-FRKDSY-----ELQVRA 202
DB 173 EPMITLLSYELAPKQSEAMQOHRDHY-----GVYMLLEAFELDPGFIHERLARLVQM 228
OY 203 GPMFG-----SYQGTWSEWDVIFQTOSEELKEGW-NPHLLLLLLLVIVFIIPAW 253
DB 229 ATLEDVVEERYTQGWSEWSQPCFOAPQPGPLIPMGMPGN--TLVAVSIFL----- 281
OY 254 SLKTHPLRLM-----KKTW--AVSPERFEMPLKYGCGSGDFKVVAGAPFTGSSLE 302
DB 282 -LITGPTLLFKLSPRVRYLFYQNVBPAPMFQPLVSVHNGFMQTMGARRAGALLSODC 340
OY 303 -----LGPWSPEVSTLEVVSCHPPRSPAKRLQLTLEQ-----PALVESDGVKPSFW 352
DB 341 AGTPQGLAEPQVQATALLTCGPAP--PKSVALEBEGEGCTRLPGULSSEVDVLPAC-- 397
OY 353 PTAQNSGSAVSEERDRPYGLVSDITVTVLDAEG--PCTWPCSCEDDGYPALDLDA-- 407
DB 398 -TEWRVQTLAVLPQED--MAPTSLTRPAPDSSGSSSSSSSSNNNNNCCALGCGYGMH 454
OY 408 LEBSPGLE-----PLLDAGTTVLSG-----GCYSAG--SPGLGSPGLSLDR 446
DB 455 LSLALPGNTQSSGPIPALACG--LSCDHQGLTQGVAVWLACHCORPGLHEDLQMWL-- 509
OY 449 LKPELADGEDM 459
DB 510 LPSVLSKARSM 520

RESULT 8

156896
gene gfi-2 protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 156896
R:Flubacher, M.M.; Bear, S.E.; Tschilis, P.N.
J. Virol. 68, 7709-7716, 1994
A/Title: Replacement of interleukin-2 (IL-2)-generated mitogenic signals by a mink cell l
ed leukemogenesis.
A/Reference number: 156896; MUID:95055995; PMID:7966560
A/Accession: 156896
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-467 <RES>
A/Cross-references: UNIPROT:Q63216; UNIPARC:UPI0000086943; GB:L36459; NID:G598371; PIDN:
C/Genetics:
A/Gene: gfi-2

Query Match 7.2%; Score 213.5; DB 2; Length 467;
 Best Local Similarity 22.0%; Pred. No. 1.2e-07;
 Matches 115; Conservative 61; Mismatches 179; Indels 167; Gaps 25;

15 OGGWGCDDLVCTYDTLQTVICILEMMNLHPSTLTLM-----QDYEELKDEAT-----SCS 66
 44 EGGKAKATGTCFNSVFRIDC---HMSA-PEPGRALHLFTSNCTDILKHKCTWDSRCT 99
 67 LHRSAHNA---THATYTCHEMDFEHFMADDFSVNITDQSGNYSQEGCSFLLAESIKPAP 122
 100 LVLPEKEAFLEPDMFTTLHRCV---MGQE---QVSLVD-----SQYLPRRHILKDP 145
 123 PENV-TYTFSGQNNISMSRSDVEDPAFWLKCKLOEYQYRGRDPMWSPRKLISYDSR 181
 146 PSDIQSNVSSGRCVLTWGISF---GLEPPLTSLSYELAFKQOEAWM-QARLKRIYGV 201
 182 SVSLPLPEFRKDSYELQVRA-----GPMSSYQGTSEMSDPIVFTQSEELKEG 233
 202 WLVLAELELNDTLYEARLRYQMLAESYDDKTEGEYKSHMSKWSQSVSFSPRKTQG- 260
 234 WNPPLLLLLL-----VIVFIPAFWSLK-THPLMRWKI-----WAVSPERPFM 278
 261 -----LILPRWQASALIVAVPILFULLTGLIHPLFRLSPKRYKRIFYQVWPSPFAFFH 312
 279 PLYGCGCGDFKRWGAFPTGSSLELGPWSPVPSTLEVYSGHPPRSPAKRLQLEDEPA 338
 313 PLYSVYHGFQTMWGARRAG----- 332
 339 ELVESDGVPRKSPFPTQNSGSAVSEERDRPYGLVSDITVTLDAEGPTCPSCDDG 398
 333 -----PQMRQDGASAPSGDSES-----STMEALATLTYSACSVQ- 367
 399 YPALDLDALEPSPGLDPLDLACTTVLSCGVAS-AGSPGLGRLGSLDLRLKPLADGE 457
 368 FPLSLKWA---TANGPFGP--PGSELVLPAGCLLEQGPSAYLP-----QE 408
 458 DMAGGLPWGGRSPGVSESEAGSFLAGLNDTTPSGFVGSQC 499
 409 DMA---PLGSARP-----PPLDSDSGSSDYCMDC 435

RESULT 9
 ZUHUR
 erythropoietin receptor precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 12-Feb-1993 #sequence revision 05-Apr-1995 #text change 09-Jul-2004
 C:Accession: A43799; A60160; A49824; A53958; A55280; I52563
 R:Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.
 Blood 76, 31-35, 1990
 A>Title: Human erythropoietin receptor: cloning, expression, and biologic characterization
 A:Reference number: A43799; MUID:90304340; PMID:2163696
 A:Accession: A43799
 A:Molecule type: mRNA
 A:Residues: 1-508 <JUN>
 A:Cross-references: UNIPROT:P19235; UNIPARC:UPI000012A0AD; GB:M60459; NID:9182244; PIDN:
 R:Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.
 Blood 76, 24-30, 1990
 A>Title: The gene for the human erythropoietin receptor: analysis of the coding sequence
 A:Reference number: A60160; MUID:90304334; PMID:2163695
 A:Accession: A60160
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA; DNA
 A:Residues: 1-101, 'R', 103-188, 'R', 191-243, 'E', 245-508 <WIN>
 A:Cross-references: UNIPARC:UPI00001736C2
 R:Noguchi, C.T.; Bae, K.S.; Chin, K.; Wade, Y.; Schechter, A.N.; Hankins, W.D.
 Blood 78, 2548-2556, 1991
 A>Title: Cloning of the human erythropoietin receptor gene.
 A:Reference number: A49824; MUID:92399733; PMID:1668606
 A:Accession: A49824
 A:Molecule type: DNA
 A:Residues: 1-508 <NOG>
 A:Cross-references: UNIPARC:UPI000012A0AD; GB:S45332; NID:9255496; PIDN:AAB23271.1; PID:
 A:Experimental source: Placenta

A>Note: sequence extracted from NCBI backbone (NCBIN:113293, NCBIPI:113294)
 R:Etremman, K.; St. John, T.
 Exp. Hematol. 19, 973-977, 1991
 A>Title: The erythropoietin receptor gene: cloning and identification of multiple tranac
 A:Reference number: A53958; MUID:91372359; PMID:1654273
 A:Accession: A53958
 A:Molecule type: mRNA
 A:Residues: 1-508 <EHR>
 A:Cross-references: UNIPARC:UPI000012A0AD
 R:Penny, L.A.; Forget, B.G.
 Genomics 11, 974-980, 1991
 A>Title: Genomic organization of the human erythropoietin receptor gene.
 A:Reference number: A55280; MUID:92147143; PMID:1664413
 A:Accession: A55280
 A:Molecule type: DNA
 A:Residues: 1-17,381-387, 'LLEQQA', 391-395,504-508 <EN>
 A:Cross-references: UNIPARC:UPI000016A8A4; UNIPARC:UPI00001736C3; UNIPARC:UPI00001736C4
 A>Note: sequence modified after extraction from NCBI backbone
 A>Note: the authors translated the codon GAT for residue 31 as B
 A>Note: an insert compared to other published sequences is considered by authors as likely
 R:Mcouch, L.; Touramille, C.; Hattab, C.; Boffa, G.; Cartron, J.P.; Chretien, S.
 Blood 78, 2557-2563, 1991
 A>Title: Cloning of the gene encoding the human erythropoietin receptor.
 A:Reference number: I52563; MUID:92399734; PMID:1668607
 A:Accession: I52563
 A>Status: translated from GB/EMBL/DBEJ
 A:Molecule type: DNA
 A:Residues: 1-96 <RES>
 A:Cross-references: UNIPARC:UPI000016A8A4; GB:M76595; NID:9182147; PIDN:AAA52393.1; PID:5;
 C:Genetics:
 A:Gene: GDB:EBOR
 A:Cross-references: GDB:125242; OMIM:133171
 A:Map position: 19p13.3-19p13.2
 A:Intons: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
 C:Superfamily: erythropoietin receptor; cytokine receptor homology
 C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-508/Domain: extracellular #status predicted <EXT>
 F:52-250/Domain: extracellular #status predicted <EXT>
 F:52-239/Domain: cytochrome receptor homology <CRS>
 F:233-237/Region: MSXMS motif
 F:251-272/Domain: transmembrane #status predicted <TM>
 F:273-508/Domain: intracellular #status predicted <INT>
 F:52-62,91-107/Disulfide bonds: #status predicted
 F:76/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 7.2%; Score 213; DB 1; Length 508;
 Best Local Similarity 21.6%; Pred. No. 1.5e-07;
 Matches 127; Conservative 63; Mismatches 175; Indels 224; Gaps 30;

9 LLLLLLGGWGC-----DLVCYDYLTQTVICILE---MMNLHP 44
 15 LCLLLAGAAWAPPNLDPKFEKALLLAAGPEELCTFERLEDVLCFMEBAASAGVGP 74
 45 STLTTLTQDQYELKDEAT-CLHRSANATATYTCM-----DVHFMDADDFSVNITD 100
 75 GNSVSFYQ-----LEDPMLKRLHQAPTARGAVFWSCLPTDTSFVP---LELVTA 126
 101 OSGVSGEGCSFLAESIKPAPPNVTF-----SQQYVISMRS 141
 127 ASG-----APRYHRYIHNEVVLDAVPGLVARLADSGHVLRPLP 169
 142 YEDPAFMYLKGKLOEYLRNRDPMWSPRKLISYDSRSVSLPLEFRKDSYELQVR 201
 170 PEP-----MTSHRYEVDVAGAGAGSV---QVEILEGRTCVLS-NLRGRTRYTAVR 221
 202 AGPMSSSYQGTSEMSDPIVFTQSEELKEGNNPHLL-----LLLVVFIIPAFWSLTKHP 259
 222 A-RAEBSFGFWMSAWSEPVSLTPSD-----LDPLTLTSLILVILVLTVALLSHR 275
 260 LMRLMKKIW-AVSPSEPFPMPLVKGCGDFPKRV-----GAPFGSSLELGPWSPPEVSTL 314
 276 R-ALKQKIMPGIISPESEFGLPTTHKGNQLMLYQNDGLW-----WSCTPFTIE 325

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QY 315 EVVSCHPRSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNNGSAYSEERDRPYGLV 374
D 326 D-----PPAS-----LEVTSERC-----MGTWQ----- 343
QY 375 SIDVTVLDAEGPCTWPCSCEDDGYPALDLAGLEPSFGLIEDPLDAGTTLVSCGVASAG 434
D 344 AVERGCT--DDEGRLFEVGEHADDTLVLDKMLPR----- 378
QY 435 SPGLGFLGLSLDLRLKPPRLADGEMMAGGLPWGGRSPGVSEASGSLAGLDMTFPSGF 494
D 379 -----NPPSEB-----LP-----GPGG-----SVDIVAMDEGS 401
QY 495 VGSPPSCSPVECDFTSPGDEG-----PPRSYLROWVPI--PP 529
D 402 EASCSALAL--SKPSPEGASASFEYTTIDPSQSILRPWTLCPDELPP 447

RESULT 10
Interleukin-3 receptor beta-subunit - rat
C/Species: Rattus sp. (rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-May-2004
C/Accession: 156563
R/Apple, K.; Buttin, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A/Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and
A/Reference number: 156563; MUID:95370942; PMID:7643220
A/Accession: 156563
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-896 <RES>
A/Cross-references: UNIPARC:UPI000008999A; GB:S79263; NID:G1086954; PIDN:AA835068.1; PIR
C/Genetics:
A/Gene: rIL-3beta
C/Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h
C/Keywords: cytokine receptor
F/23-235/Domain: cytokine receptor homology <CRS1>
F/23-433/Domain: cytokine receptor homology <CRS2>

Query Match 7.2%; Score 211.5; DB 2; Length 896;
Best Local Similarity 21.7%; Pred. No. 3.8e-07;
Matches 126; Conservative 79; Mismatches 228; Indels 147; Gaps 28;

QY 2 PRGMAALLLLLOGMGCP-----DLVCTDYDTQVCIEMNNLHPSITLTMQD 53
D 229 PSCGSPV-----HWDSPTEKARPONLQCFDGIQSLNCSWEVWTKVTDVSFGLFY 281
QY 54 QYELKDEATSCSLHRSAHNATHATYCHMDVFHFMADDIPSVNITDQSGNYSGEGSFL 113
D 282 SSSPKAGEKCSFVVKELQASRYTRHCSLNVSDPAHSAQYTSVK-----RLQCKFI 335
QY 114 LA-ESIKPAPP-FNVTYTFSGQYNI SMSDYEDPAFYWLKGLQYELQYRNRRGDPWAVSP 171
D 336 ESFNHIQNPPTLNLTKN-RDSYSLHMETQMSYFI----QHAFQYQKKKLLRWEDESK 390
QY 172 RKLLISVDSRSVSLPLERKDSYELQYRAGMPGSSYQGTWSEMSPVVIFQOSEBK 231
D 391 TENLNHAHSMQ--LP-QLEPGTSYCARVRKTP--EYKGLMSESECTWTDD----- 439
QY 232 EGM-NPHL--LILLVIVFIPA--FWSLTHPLMLMKIMAVSPERPFMLYKCS 285
D 440 --WMPFLMVLIVLITLTLRLRFGCIYCKLIRMKKIKINPSLSLFOGGKGL- 496
QY 286 GDFKRWGAPFTGSLBLGPMSPVPSLVEYSCHP--PRSPAKRLQLTLEQPAELVESD 344
D 497 -----WPP--GSTVTFSSKNPFPQGPQNL--FSEIQ----- 524
QY 345 GVKPSFWPTAQNNGSAYSEERDRPYGLVSDIVTVL--DAEGPCTWPCSCEDDGYPAL 402
D 525 -----GVSYTHLEDNVSPPLTIEDPNIIRDPSSGDPDTTPAASSBP----- 564
QY 403 DLDAGLEPSPGLE-DPLLDAGTTLVSCGVASGFLGGLP-----GSLLD-----R 448
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D 565 -----MEQSNVQVDEPTLSGRPRKQLPSFDFNGPYLGPQSHSLDLPQOLVPGGVGS 619
QY 449 LKRPRLADGEMMAGGLPWGGRSPG-----VSESEKSGSLAGLDMTFPSGFVGS 498
D 620 LKRAL-----PSLSELMCLPFGGQVQLVPLSCVMKQGRVDVQCSSLETSPSEMR 673
QY 499 CSSPVECDFTSPGDEGPPRSYLROWVPIPPLSPPQAS 538
D 674 ESPPELV-----KEBQEPKRN-----PYTLPISSGGPKDS 704

RESULT 11
cytokine receptor common beta chain precursor - human
A/39255
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-May-2004
C/Accession: A39255
R/Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A/Title: Molecular cloning of a second subunit of the receptor for human granulocyte-mac
A/Reference number: A39255; MUID:91086571; PMID:1702217
A/Accession: A39255
A/Molecule type: mRNA
A/Residues: 1-897 <RAY>
A/Cross-references: UNIPARC:UPI00001736C0; GB:M38275
C/Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
C/Genetics:
A/Gene: GDB:CSF2RB
A/Cross-references: GDB:126838; OMIM:138981
A/Map position: 22q13.1-22q13.1
C/Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h
C/Keywords: alternative splicing; cytokine receptor; duplication; transmembrane protein
F/1-16/Domain: signal sequence #status predicted <Sig>
F/1-897/Product: cytokine receptor common beta chain #status predicted <MAT>
F/17-443/Domain: extracellular #status predicted <EXT>
F/35-222/Domain: cytokine receptor homology <CRS1>
F/250-431/Domain: cytokine receptor homology <CRS2>
F/444-460/Domain: transmembrane #status predicted <TM>
F/461-897/Domain: intracellular #status predicted <INT>

Query Match 6.3%; Score 204; DB 1; Length 897;
Best Local Similarity 22.6%; Pred. No. 1.3e-06;
Matches 142; Conservative 66; Mismatches 219; Indels 200; Gaps 32;

QY 22 DLVCTDYDTQVCIEMNNLHPSITL--LTMDQYBELKDEATSC-----SLHRSAH- 72
D 247 NLRCFPDGAALVLCSMWEKREVASVSGFLYKPSDPAGEECSPVLREGLSLHTRHHC 306
QY 73 -----NATHATYCHMDVFHFMADDIPSVNITDQSGNYSGEGSFLAESIKPAPPNV 126
D 307 QIYVPRPATHTGY-----IVSV-----QPRRAKHKS---SVNIGMAP--SL 345
QY 127 TYTFSG-QYNIW-----RSYEDPAFYWLKGLQYELQYRNRRGDPWAVSPRKLISVDS 180
D 346 NVTKDGSYSLSRWEIWKMRYEIHDTF-----EIQYKDTATWKSDETL--QNA 394
QY 181 RYSVSLPLERKDSYELQYRAGMPGSSYQGTWSEMSDPVITQOSEBKDEGNPHLL 240
D 395 HSMALPALE--PSTRWARVRV-RTSRTGNGIWMSESESRSDTES--VLPMW----- 443
QY 241 LILLVIVFIPA-----FWSLTHPLMLMKIMAVSPERPFMLYKCSGDPFKW-- 291
D 444 VIALIVIFLTTAVLALRLRFGCIYCKLIRMKKIKINPSLSHIFQ-----NSAELMPP 497
QY 292 --VGAPFTGSLBLGPMSPV-----PSLSE--VYSCHPSPSPAKRLQ 330
D 498 GMSAFTSGSPRPHQGPWGRFPELGVFPVGFDSSEVSLTIDPKHVCDDPSPGPTTPA 557
QY 331 LTELQPAELVESDGVKPSFWPTAQNNGSAYSEERDRPYGLVSDIVTVLDAEGCTW 390
D 558 ASDLPTEQPSPPGPPPAASHTEKQAS-----FPNGGYLG 595
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QY 138 WRSDYEDPAFYMLKGLQYELQYRNRGDPAVSPRRKLISVDSRSVSLPLEFRKDSYE 197
Db 182 -----DVSAGNR-----AGCTQREVELEGRECVLS-NLKGRTY 216
QY 198 LQVACGMPGSSYOGTSEMSDPVIPTQOSELEKEGNPHLLLLLVTFIP---AFWS 254
Db 217 PAVNA-RMAEPPGFPMSAMSEPAISLTAAD-----LDP-LILVLSLVLISLITVLA 269
QY 255 LKTHPLRLMKKIV-AVSPERFPMPLKGGSGDFKVV---GAPFTGSSLEIGPMSPE 309
Db 270 LLSHRR-ALROKIVPGIPSPENEEGGLFTTHKGNFQMLLQRDGLW-----WSPS 319
QY 310 VPSLLEYVSSCHPMSPAKRLQLEQEBALVESDGVKPSFWPTAQNSSGSAVSEERD- 368
Db 320 SPF-----PEDPPALHEVLSERR-----WGYTQ--AGDAGAEKGP 353
QY 369 --RPYGLV-SIDTPTVLDAEGPCTW-----PCSGCEDDYPALDLDALEPSPGLEPDL 420
Db 354 LLEVGSEBRADDTLVLD-----EMLPRCPCSENLSG-----PGDSVDPATMD 397
QY 421 AGTTVLSGCVSAGSPGLG-----PLGSLI-DRLKPPDLADGEDMAGGLPWG 467
Db 398 EGSETSSCPSDIAKPPPEGTSPSFEYTIIDPSSKLLCPRALPP----- 442
QY 468 RSPGVSESEAKSP-LAGLMDTDFDSGFVSGDCSSPVCEPFGDEG 514
Db 443 -----ELPPTPHLLKLYLVVSDSG-----ISTDYSGGSG 474

RESULT 14
A60386
interleukin-4 receptor precursor - human
N:Alternate names: IL-4 receptor
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
A:Accession: A60386; MUID:91120547; PMID:2278997
R:Galizzi, J.P.; Zubur, C.E.; Harada, N.; Gorman, D.M.; Djossou, O.; Kaetelein, R.; Banc
Int. Immunol. 2, 669-675, 1990
A:Title: Molecular cloning of a cDNA encoding the human interleukin 4 receptor.
A:Reference number: A60386; MUID:91120547; PMID:2278997
A:Accession: A60386
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-825 <GAL>
A:Cross-references: UNIPROT:P24394; UNIPARC:UPI0000169C06
R:Idzerda, R.L.; March, C.J.; Mosley, B.; Lyman, S.D.; Vanden Bos, T.; Gimpel, S.D.; Dir
J. Exp. Med. 171, 861-873, 1990
A:Title: Human interleukin 4 receptor confers biological responsiveness and defines a nc
A:Reference number: A47603; MUID:90171849; PMID:2307934
A:Accession: A47603
A:Molecule type: mRNA
A:Residues: 1-74, 'I', '76-825 <ID2>
A:Cross-references: UNIPARC:UPI0000044371; GB:X52425; NID:G33833; PIDN:CAA3672.1; PID:G
C:Genetics:
A:Gene: GDB:1148
A:Cross-references: GDB:118823; OMTM:147781
A:Map position: 16p12.1-16p12.1
C:Superfamily: interleukin-4 receptor; cytokine receptor homology
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-825/Product: interleukin-4 receptor #status predicted <MNT>
F:26-222/Domain: extracellular #status predicted <EXT>
F:23-218/Domain: cytokine receptor homology <CRS>
F:223-256/Domain: transmembrane #status predicted <TM>
F:257-825/Domain: intracellular #status predicted <INT>
F:53,98,128,134,146,209/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.5%; Score 193.5; DB 1; Length 825;
Best Local Similarity 21.8%; Pred. No. 6.6e-06;
Matches 161; Conservative 69; Mismatches 220; Indels 289; Gaps 42;
QY 17 GWGCPDLV-----CTDLYQTVICILMEMNLHNPST-----L 47

Db 2 GMLCSGLLPFVSCVLTLQVASSGNMKVLOEPTCVSDYMSISTC---EMKNNGPTNCSTEL 58
QY 48 TLTWQDOYEELKBKATSCSLHRSANAHATYTCCHMVFHFMADDFSVNITQSGNYSQ 107
Db 59 RLIVYQLVF--LLEAHLC-----VPENNNGAGCVCHL-----LMDVVASD-----NYTL 101
QY 108 EC-----GSFLAESIKPAPPFNVTV--TFSGQYNISWRSYEDDPAFYMLKGLQY 156
Db 102 DLWAGQQLMKWGSFKPSEHVKPPAPGULTYHTVNSDTLLTWSNPY--PDDNLYNHLTY 159
QY 157 ELQYRNKGDPAVSPRRKLISVDSRSVSLPLE-----FRKSSYELQVRAGMPG 207
Db 160 AVNIMSNDP-----ADFRIYNYVYLEPSLRIAASTLKSGISYARAVAW---A 205
QY 208 SSTQGTSEMSDPVIPTQOSELEKEGNPHLLLLLVIFIPAFMSLKTHPLRLMKKI 267
Db 206 QCVNTTWSEMSPTKWH--NSYREPEQHLHGVSVSCIVLAVCLLCVYSTIKIKKEW 262
QY 268 W-AVSPERPFM-----PLYKGC-----S 285
Db 263 WDIQIPNAPARLVAIIITQDAQSGSWEKRSRQERPAKCPHKNTKLLPCGLEHMKRDE 322
QY 286 GDFKRWGAPFTGSSLELGPMSF-EV-----PSTLEVYSCHPPRSPAKRLQLEQ-P 337
Db 323 DPHKAKEMFFQSGG--KSAMCPVEISKVILMPESISVAVC-----VELFEAP 368
QY 338 AELVESDGV--PKRSPFWPTQNSSGSAVSEERDRPYGLVSDITYTV-LDAG----- 386
Db 369 VCEEEEEEVEEEKSFCASSPSSRD--FOGRE--GIVARLTESLFLDLLEENGSGFCQ 424
QY 387 -----PCTWPCSCED-----DGYPALDLDAE-----LEPSPG----- 413
Db 425 QDMGESCLLPSPSGSTSHMWDEPFS---AGREKAPMKGEORLHEPSPASPTQSPD 480
QY 414 ----LBDPLLDAGTV--LSCGCVSAGSPGLGP--LGSLLDRLKP----- 451
Db 481 NLCTERPLVIAGNPAVRSFNSLSQSPCRELGPDLRLARHLEVEPEMPCVQLSEPT 540
QY 452 --PLADSEDM-----AGGLPMWGRSRG---GVSESEAG-----SPPLGL----- 485
Db 541 TVPQPEPETWEQILRRNVLQHGAAPVAPVSAPTSGYGFVHAVQGGTQASAVVGLGPGE 600
QY 486 -DMDTDFDSGFVSGDCSSPVCEPFGDFTS-----PDDEGPPRSYLKQWVIP 527
Db 601 AGYKAF--SSLASAVSEKCGFCASSGEGYKPFQDLIGCCFEDPAP-----VP 649
QY 528 PPLSSPG-----PGAS 538
Db 650 VPLFTFGLDREPPRSQSS 668

RESULT 15
A33380
interleukin-4 receptor precursor - mouse
N:Alternate names: IL-4 receptor
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
A:Accession: A33380; B33380; C33380; A34861; I54232
R:Mosley, B.; Beckmann, M.P.; March, C.J.; Idzerda, R.L.; Gimpel, S.D.; VandenBos, T.; F
Widmer, M.B.; Coelman, D.; Park, L.S.
Cell 59, 335-348, 1989
A:Title: The murine interleukin-4 receptor: molecular cloning and characterization of seq
A:Reference number: A90911; MUID:90030408; PMID:2805066
A:Accession: A33380
A:Molecule type: mRNA
A:Residues: 1-810 <MO1>
A:Cross-references: UNIPROT:P16382; UNIPARC:UPI000004194; GB:M27959; NID:G198363; PIDN:J
A:Accession: B33380
A:Molecule type: mRNA
A:Residues: 1-258 <MO2>
A:Cross-references: UNIPARC:UPI00001736C1

A:Molecule type: mRNA
 A:Residues: 1224, 'PSNENL', <MO3>
 A:Cross-references: UNIPARC:UPI000001736C1; GB:M27960; NID:g198365; PIDN:AAA39300.1; PID:
 A:Note: part of this sequence, including the amino end of the mature protein, was confir
 A:Note: three forms of cDNA were isolated; the longest encodes extracellular, transmembr
 A:Note: domain and may encode a soluble form of the receptor
 R.Harda, N.; Castelle, B.E.; Gorman, D.M.; Itoh, N.; Schreure, J.; Barrett, R.L.; Howard,
 Proc. Natl. Acad. Sci. U.S.A. 87, 857-861, 1990
 A>Title: Expression cloning of a cDNA encoding the murine interleukin 4 receptor based c
 A:Reference number: A34861; MID:90138976; PMID:2405398
 A:Accession: A34861
 A:Molecule type: mRNA
 A:Residues: 1-810 <HAR>
 A:Cross-references: UNIPARC:UPI0000004194; GB:M29854; NID:g198346; PIDN:AAA3297.1; PID:
 R.Wrighton, N.C.; Campbell, L.A.; Lee, F.D.
 Growth Factors 6, 103-118, 1992
 A>Title: The murine interleukin-4 receptor gene: Genomic structure, expression and pote
 A:Reference number: 154232; MID:92265335; PMID:1534014
 A:Accession: 154232
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-73, 'I', '75-333', 'P', '335-810' <RES>
 A:Cross-references: UNIPARC:UPI00000655CA; GB:M64879; NID:g198359; PIDN:AAB59727.1; PID:
 C:Genetics:
 A:introns: 24/1; 71/2; 122/1; 172/3; 225/1; 258/2; 284/3; 301/2
 C:superfamily: interleukin-4 receptor; cytokine receptor homology
 C:keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-810/Product: interleukin-4 receptor #status experimental <MAT>
 F:26-233/Domain: extracellular #status predicted <EXT>
 F:24-219/Domain: cytokine receptor homology <CRS>
 F:234-257/Domain: transmembrane #status predicted <TM>
 F:258-810/Domain: intracellular #status predicted <INT>
 F:72,129,135,163,177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.4%; Score 189.5; DB 1; Length 810;
 Best Local Similarity 20.9%; Pred. No. 1.3e-05;
 Matches 159; Conservative 70; Mismatches 222; Indels 309; Gaps 42;

QY 9 LLLLLLQGGWGCPLD---VCYTYLQTVICILEMWNH-----PSTLTTLTQDOYEELKD 60
 DB 15 LILLLVATGSGSIVLGEPTCFSDYIRSTC---EMFLDSAVDCSQCLHYRLMFFEFSE 71
 QY 61 EATSCSLHRSANATATYTCGMDVFRHMADIFSVNITDQSGNYSQEC-----GS 111
 DB 72 NLTCI-----PRNSASTVCVCHME-----NMRPVQSDRYQWELMAEHRQLWGS 115
 QY 112 FLAESTIKPAPPNVTY--TFSGQYNISWRSDY-----EDPAPYML 150
 DB 116 FSPSGNVKPLAPNLTLLHTVSDMLTNNLTPSNLLYKDLISMVNIREDNPAPFIV 175
 QY 151 KGLQYELQYRNKGDPAVSPRRKLISVDSRSVSLPLEFRKDSYELQVRAGMPGSSY 210
 DB 176 ---YNVTYK---EPRLSPFINILMS-----GVYYTARVR---VRSQIL 209
 QY 211 QGTWSEKSDPVITQTOSEELKEGNNPHLLLLL-----LVVFTPAFWSLKTPLMR 262
 DB 210 TGTWSEWSPSIT-----WYNHFOPLIQRPLGVITISCLCIPFLCFYFSITX 258
 QY 263 LMKKIW--AVSPERPFM-----PLYKGC----- 284
 DB 259 I-KKIWMDOQIPTPRSPVAIIITQDAQPLMDKQTRSQESTKYPHWKTCLDKLLPCLLK 317
 QY 285 ---SGDFKMGVAGPFTGSSLELGP--WSP-EVPSLELVYSCPPRSPAKRLQLTLEOE- 336
 DB 318 RVKKKTDPRK--AAP-TKLSQSPGKAGMCMEVSRIV---LWPEVSVSVRCMELFEA 370
 QY 337 PAELV--ESGCVPRKPSFWPTAQNSSGSAYSB-EKDRPYGLVSDITVTVLDAE----- 385
 DB 371 PVQNVBEEDBEIVKEDLSMSPENSGCGFQSSQADIMARLTENLFSDLLEAENGLQCSA 430
 QY 386 -----GPTWPC-----SCBDDGVPAULDLDAGLEPSPGLDPLDAG 422

DB 431 LAESCPLPSGSGQASVSWACLPMGPSEBATTQVTEQPS-----HPGLSGSPAQSA 483
 QY 423 TTVLSG-----CVSAGSPGLGGPLGSLDLRLK----- 450
 DB 484 T-LACTQVPLVADNPAYRSFSDCCSPAPNPGELAPBEQQADHLEEEPPSPADPHSSG 541
 QY 451 PPLADGEDW-----AGG--LPMGSG-----RSPGVSESEAGSP 481
 DB 542 PPMQPVESMEQLHMSVLQHGAAAGSTPAPAGGYQGFVQAVKQGAADPEVPGVRPSGDP 601
 QY 482 -----LAGLMDT---FDSGFVG-----SDCSPVECDFT----- 508
 DB 602 GYKAFSSLLSNIGRDTAAAGTDDGHGGYKPFQNPVPMQSPSSVPL---FTGGLDTELS 658
 QY 509 -SPGDGPPRPSYLR-----QWVVIPEPLSS-PCP 535
 DB 659 PSLNSDPPKSPPECGLGLEIGLKGDWVXAPPPADQVPRK 698

Search completed: September 7, 2006, 12:52:23
 Job time : 43.1971 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:40:11 ; Search time 296.669 Seconds
(without alignments)
1677.489 Million cell updates/sec

Title: US-10-659-684-115

Predict score: 2958
Sequence: 1 MFGMAAPLILLLLQGSGWC.....YLRQWVIVPPPLSSPQAS 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 7.2:*
1: UniProt_sprot:*
2: UniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2958	100.0	538	1 IL21R_HUMAN	O9HBE5 homo sapien
2	1735.5	58.7	529	1 IL21R_MOUSE	O9JHX3 mus musculu
3	1735.5	58.7	529	1 O3TA13_MOUSE	O3TA13 mus musculu
4	1734.5	58.6	529	2 O3UBS8_MOUSE	O3UBS8 mus musculu
5	1703.5	57.6	521	2 O5EBH1_RAT	O5EBH1 rattus norv
6	1082	36.6	292	2 O3TA82_MOUSE	O3TA82 mus musculu
7	872	29.5	268	2 O6FEU8_MOUSE	O6FEU8 mus musculu
8	764	25.8	590	2 O5F4A6_CHICK	O5F4A6 gallus gall
9	294	9.9	551	1 IL2RB_MACFA	O38J85 macaca fasc
10	286	9.7	512	2 O6UAP3_TETNG	O6UAP3 tetradon n
11	280	9.5	551	1 IL2RB_PANTR	O38J84 pan troglod
12	278	9.4	551	1 IL2RB_HUMAN	P14788 homo sapien
13	261	8.8	509	2 Q2VBO8_BRARE	Q2VBO8 brachydantio
14	250	8.5	890	2 O9Z1A0_CAVPO	O9Z1A0 cavia porce
15	248	8.4	537	1 IL2RB_RAT	P68896 rattus norv
16	247.5	8.4	539	1 IL2RB_MOUSE	O3T2C2 mus musculu
17	247.5	8.4	539	2 O3TRT2_MOUSE	O3TRT2 mus musculu
18	246.5	8.3	539	2 O3TB02_MOUSE	O3TB02 mus musculu
19	245.5	8.3	539	2 O8R308_MOUSE	O8R308 mus musculu
20	243.5	8.2	539	2 O8CB01_MOUSE	O8CB01 mus musculu
21	239.5	8.1	539	2 O4KKX7_MOUSE	O4KKX7 mus musculu
22	233	7.9	896	1 IL3RB_MOUSE	P26955 mus musculu
23	231	7.8	896	2 O3U7L5_MOUSE	O3U7L5 mus musculu
24	231	7.8	896	2 O8QZK9_MOUSE	O8QZK9 mus musculu
25	231	7.8	896	2 O3U2T6_MOUSE	O3U2T6 m nod-deriv
26	227	7.7	896	2 O3UI09_MOUSE	O3UI09 mus musculu
27	226	7.6	529	2 O6UAP7_TETNG	O6UAP7 tetradon n
28	221.5	7.5	468	1 IL9R_MOUSE	O01114 mus musculu
29	221.5	7.5	468	1 O78PA5_MOUSE	O78PA5 mus musculu
30	221.5	7.5	631	2 O6UANA_TETNG	O6UANA tetradon n
31	221.5	7.5	878	2 O3UIW0_MOUSE	O3UIW0 mus musculu

32	221.5	7.5	878	2 O3U2A1_MOUSE	O3U2A1 m nod-deriv
33	218.5	7.4	439	2 O6UAG6_TETNG	O6UAG6 tetradon n
34	218.5	7.4	769	2 O3UIZ1_MOUSE	O3UIZ1 mus musculu
35	218.5	7.4	790	2 O3UIP4_MOUSE	O3UIP4 mus musculu
36	218.5	7.4	878	1 IL3B2_MOUSE	P26954 mus musculu
37	215	7.3	522	1 IL9R_HUMAN	O01113 homo sapien
38	213.5	7.2	467	2 O63216_RAT	O63216 rattus norv
39	213	7.2	508	1 EPOR_HUMAN	P19235 homo sapien
40	213	7.2	508	2 Q2M205_HUMAN	Q2M205 homo sapien
41	211.5	7.2	896	2 O64146_9MURI	O64146 rattus sp.
42	211.5	7.2	896	2 O782F5_RAT	O782F5 rattus norv
43	210	7.1	469	2 O8C2G1_MOUSE	O8C2G1 mus musculu
44	208.5	7.0	652	2 O3UI24_MOUSE	O3UI24 mus musculu
45	208.5	7.0	670	2 O3TB34_MOUSE	O3TB34 mus musculu

ALIGNMENTS

RESULT 1
ID IL21R_HUMAN STANDARD; PRT; 538 AA.
AC O9HBE5; O96H21; O9HB91;
DT 02-MAY-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DT 07-MAR-2006, entry version 47.
DE Interleukin-21 receptor precursor (IL-21R) (Novel interleukin
DE receptor).
GN Name=IL21R; Synonyms=NILR; ORFNames=UNQ3121/PRO10273;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;
RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
RA Grose J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
RA Burkhead S., Hejblum M., Brandt C., Kuiper J.L., Kramer J.,
RA Conklin D., Pressnell S.R., Berry J., Shiota F., Bort S., Hamblly K.,
RA Mdridi S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer M., Kaushansky K., Holly R.D., Foster D.;
RT "Interleukin 21 and its receptor are involved in NK cell expansion and
RT regulation of lymphocyte function.";
RL Nature 408:57-63 (2000).
[2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20481926; PubMed=11016959; DOI=10.1073/pnas.200360997;
RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.U.;
RT "Cloning of a type I cytokine receptor most related to the IL-2
RT receptor beta chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444 (2000).
[3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Bruen J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Lao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
RA Yarusu D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270 (2003).
[4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS CYS-191; ARG-318 AND
RP SER-484.

RA Bieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Peol C.L., Toch E.V., Yi Q., Nickerson D.A.;
RT "SeattleSNP: NHLBI H66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA URL: <http://pga.gs.washington.edu/>;"
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=B-cell, and Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP PROTEIN SEQUENCE OF 20-34.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
CC -1- FUNCTION: This is a receptor for interleukin-21.
CC -1- SUBUNIT: Heterodimer with the common gamma chain. Associates with
CC JAK1.
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -1- TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues.
CC Most highly expressed in thymus and spleen.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 4
CC subfamily.
CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC
CC EMBL: AF254067; AAC29346.1; -; mRNA.
CC EMBL: AF269133; AAC23419.1; -; mRNA.
CC EMBL: AY358826; AAC09185.1; -; mRNA.
CC EMBL: AY064474; AAL39168.1; -; Genomic_DNA.
CC EMBL: BC004348; AAH04348.1; -; mRNA.
CC EMBL: BC007946; AAH07946.2; -; mRNA.
CC HSSP: P19235; 1EBA.
CC Ensembl: ENSG00000103522; Homo sapiens.
CC DR H-InvDB: HIX0012913; -;
CC DR HGNC: HGNC:6006; IL21R.
CC DR MIM: 605383; gene.
CC DR GO: GO:0016021; C:integral to membrane; NAS.
CC DR GO: GO:0001532; P:interleukin-21 receptor activity; NAS.
CC DR GO: GO:0030101; P:natural killer cell activation; NAS.
CC DR InterPro: IPR003531; FN_III.
CC DR InterPro: IPR003531; FN_III.
CC DR PROSITE: PS50853; FN3; FALSE NEG.
CC DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.

KW Direct protein sequencing; Glycoprotein; Membrane; Polymorphism;
KW Receptor; Signal; Transmembrane.
FT SIGNAL 1 19
FT CHAIN 20 538
FT
FT TOPO_DOM 20 232
FT TRANSMEM 233 253
FT TOPO_DOM 254 538
FT DOMAIN 120 209
FT MOTIF 214 218
FT CARBOHYD 73 73
FT CARBOHYD 97 97
FT CARBOHYD 104 104
FT CARBOHYD 125 125
FT CARBOHYD 135 135
FT DISULFID 25 35
FT DISULFID 65 81
FT VARIANT 191 191
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FT VARIANT 318 318
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FT VARIANT 484 484
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FT CONFLICT 386 386
FT SEQUENCE 538 AA; 59130 MW; 414079CCB974850A CRC64;
Query Match 100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 7,8e-203; Mismatches 0; Indels 0; Gaps 0;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MPKGMAAPLILLLLGGGMCPCDLYCYTDYQYICILEMNNLHPSTLTLMODQYEELKD 60
1 MPKGMAAPLILLLLGGGMCPCDLYCYTDYQYICILEMNNLHPSTLTLMODQYEELKD 60
61 EATSCSLHRSANAHATATYTCNDVDFHFNADIFSVNITDQSGNYSQEGCSFLAESIKP 120
61 EATSCSLHRSANAHATATYTCNDVDFHFNADIFSVNITDQSGNYSQEGCSFLAESIKP 120
61 EATSCSLHRSANAHATATYTCNDVDFHFNADIFSVNITDQSGNYSQEGCSFLAESIKP 120
121 APPENVTVTSSGQYNTSMRSYEDYEDPAFYMLKGLQYELQYRNKGDPVAVSPPRKLISVDS 180
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181 RVSLLPLERKSSVELQYRAGPMGSSYQGTWSEMSDVIRPOTQSEELKEGNPILL 240
181 RVSLLPLERKSSVELQYRAGPMGSSYQGTWSEMSDVIRPOTQSEELKEGNPILL 240
241 LLLLVIVFIPAFWSLKTHTPLMLMKKIWAAPSEBPFMPDYKGGSGDFKMGVGAFTGSS 300
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241 LLLLVIVFIPAFWSLKTHTPLMLMKKIWAAPSEBPFMPDYKGGSGDFKMGVGAFTGSS 300
301 LEIGPMSPEVPSLTLEVSSCHPSPSPAKRLOLTLEQEAELVESDGVKPSFWPNAQNSCG 360
301 LEIGPMSPEVPSLTLEVSSCHPSPSPAKRLOLTLEQEAELVESDGVKPSFWPNAQNSCG 360
301 LEIGPMSPEVPSLTLEVSSCHPSPSPAKRLOLTLEQEAELVESDGVKPSFWPNAQNSCG 360
361 SAYSEERDRPYGLVSTDTVTVLAEGPCPTWPCSCEDDGYPALDADLSPSPGLEEDLLD 420
361 SAYSEERDRPYGLVSTDTVTVLAEGPCPTWPCSCEDDGYPALDADLSPSPGLEEDLLD 420
361 SAYSEERDRPYGLVSTDTVTVLAEGPCPTWPCSCEDDGYPALDADLSPSPGLEEDLLD 420
421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLPLADGDMWAGLPMWGRSPGVSESEBAGS 480
421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLPLADGDMWAGLPMWGRSPGVSESEBAGS 480
421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLPLADGDMWAGLPMWGRSPGVSESEBAGS 480
481 PLAGLMDTDTDSGFGVSDCSSPVCEPDTSPGSDGPPRSYLRQWVVIIPPLSPSPQAS 538
481 PLAGLMDTDTDSGFGVSDCSSPVCEPDTSPGSDGPPRSYLRQWVVIIPPLSPSPQAS 538
481 PLAGLMDTDTDSGFGVSDCSSPVCEPDTSPGSDGPPRSYLRQWVVIIPPLSPSPQAS 538
RESULT 2
ID121R_MOUSE STANDARD; PRT; 529 AA.
AC Q9UHX3; Q9ESM1;
DT 02-MAY-2002, integrated into UniProtKB/Swiss-Prot.

01-OCT-2000, sequence version 1.
07-MAR-2006, entry version 39.
Interleukin-21 receptor precursor (IL-21R) (Novel interleukin receptor) (Lymphocyte receptor beta) (IL-beta) (Novel cytokine receptor NR8).
Name=IL21r; Synonyms=NLlr;
Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
[1]
NP NUCLEOTIDE SEQUENCE [mRNA].
RC STRAIN=C57BL/6;
RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;
RA Parish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Brandt C., Kuiper J.L., Kramer J., Conklin D., Preneil S.R., Berry J., Shiota F., Bort S., Hamblly K., Murti S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., RA Maurer M., Kaushansky K., Holly R.D., Foster D.;
RT "Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function.";
RT Nature 408:57-63(2000).
[2]
NP NUCLEOTIDE SEQUENCE [mRNA].
RC TISSUE=Spleen, and Thymus;
RX MEDLINE=20481926; PubMed=11016959; DOI=10.1073/pnas.200360997;
RA Oraki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;
RT "Cloning of a type I cytokine receptor most related to the IL-2 receptor beta chain.";
RT Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).
[3]
NP NUCLEOTIDE SEQUENCE [mRNA].
RA Donaldson C.D., Whitters M.J., Fitz L., Unger M., Finerty H., Dagdigan C., Lowe L., Wood C.R., Young D.A., Collins M.;
RT "Chromosome 16p12 encodes a biologically active IL-2Rb related receptor with lymphoid restricted expression.";
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
[4]
NP NUCLEOTIDE SEQUENCE [mRNA].
RC STRAIN=BALB/c;
RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
RT "A novel cytokine receptor NR8 is closely mapped to IL-4R: polymorphism in Balb/c mouse.";
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[5]
NP NUCLEOTIDE SEQUENCE [mRNA].
RC STRAIN=A/J, B10.S/DvTe, C57BL/6J, NOD/LtJ, and SJL/J; TISSUE=Spleen;
RA Gao J., Teuscher C.;
RT "Mus musculus interleukin 21 receptor gene 1121r mRNA.";
RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
[6]
NP NUCLEOTIDE SEQUENCE [mRNA].
CC -1- SUBUNIT: Heterodimer with the common gamma chain. Associates with JAK1.
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane protein.
CC -1- TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues.
CC -1- Most highly expressed in thymus and spleen.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or activation.
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 4 subfamily.
CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC EMBL, AF254068; AAC29347.1; -; mRNA.

DR EMBL: AF269134; AAC23420.1; -; mRNA.
DR EMBL: AF279436; AAF6350.1; -; mRNA.
DR EMBL: AB049137; BAB13736.1; -; mRNA.
DR EMBL: AF477982; AAL82632.1; -; mRNA.
DR EMBL: AF477983; AAL82633.1; -; mRNA.
DR EMBL: AF477984; AAL82634.1; -; mRNA.
DR EMBL: AF477985; AAL82635.1; -; mRNA.
DR EMBL: AF477986; AAL82636.1; -; mRNA.
DR Ensemble; ENSMUSG0000030745; Mus musculus.
DR MGI; MGI:1890475; 1121r.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004907; F:interleukin receptor activity; IDA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003531; Hempr_xcpt_S_F1.
DR PROSITE; PS00853; FN3; FALSE_NEG.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Glycoprotein; Membrane; Polymorphism; Receptor; Signal; Transmembrane.
FT SIGNAL 1 19
FT CHAIN 20 529
FT TOPO_DOM 20 237
FT TRANSMEM 238 258
FT TOPO_DOM 259 529
FT DOMAIN 120 209
FT MOTIF 214 218
FT MOTIF 266 274
FT CARBOHYD 73 73
FT CARBOHYD 97 97
FT CARBOHYD 104 104
FT CARBOHYD 125 125
FT CARBOHYD 182 182
FT DISULFID 25 35
FT DISULFID 65 81
FT VARIANT 69 69
FT VARIANT 200 200
SQ SEQUENCE 529 AA; 58355 MW; 8B41816BD0426581 CRC64;
Query Match 58.7%; Score 1735.5; DB 1; Length 529;
Best Local Similarity 62.7%; Pred. No. 2e-115;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;
QY 1 MPKGMAAPLLLLLLGGMGCEPDVLCYDTVQVCIEMNNLHPSTYTLTQDQYEBLKD 60
DB 1 MPKGPVALLLLLIHGMSCDLTCYTDYLTITCVLETSPNISLSLTQDYEYELQD 60
QY 61 EATSCSLHRSANNAHTATYTCNDVHFHMADDFSVNITDQSGNYSGECGFFLLAESIKP 120
DB 61 QETFCSLHRSGHNTHTIWTCHMRLSQFLSDEVITVVTQSGNNSQECGFFLLAESIKP 120
QY 121 APPPNVTVTSSGQYINISWRSDYEDPAFYMLKGLQIELOQRNRGDPMAVSPRRKLISVDS 180
DB 121 APPPLNVTVAASGRYDISMDASAYDEPSNVYLRGKLQYELQYRNLRDPAVVRVTLISVDS 180
QY 181 RVSLSLPLFRKQSSVYELQYRAGPMGSSYOGTWSMSDPYIFOTQSEELKEGNNPHLL 240
DB 181 RNVSLPLRBEFRKQSSYQLOVRAADQPGTSFRGTSEMSDPYIFOTQGEFPAGADPHKL 240
QY 241 LLILVIFIPAFWSLKTHTPLRMKKIWA-VPSBERFPMPLYYKCGSDPKKMGAPPTGS 299
DB 241 LLAVLLIIVL-VFMGLKHLPMRLMKKIWAPVPRESFFQPLYRHSNGFKKMWVTPFTAS 299
QY 300 SLEIGPMSPVPEVPTLEVYSCHPPSPAKRIQLTELQPAELVSDVYPKPSFW--PTAQ 356
DB 300 SIELVPOSSSTTTSL-----HLSLYPAKKKKFPLPLLEQQLLEDGMSPEGMWCIPLAA 354
QY 357 NSGGSAYSEBRDRYGLVSDITVTLDABEGCTPSCCEDDGYALDGLBSPGLAD 416
DB 355 GQAVSAISSEBRDRYGLVSDITVTLDABEGLCVWPCCEBDGIPAMMLDAGRESGPNSED 414
QY 417 PLIDAGTTVSSCGCVSAGDGLGSLDLRLKPLPLADEDVAGGLPMGGRSPGVSES 476
DB 415 LLIVTDPAFLSCGCVSSGSLRIGSSPGSLDLRLKPLAKGSDWADPTWRTGSGGSES 474

Oy	477	ENAGSLPAGLDMNTPOSGFAGSDCCSSEVCEDFTSRPGEGPRRTXLRQWVYPPPLSSGCPQ	536
Db	475	EAGSG-PGIDMDTDFSGFAGSDCCSSEVET-----DEGPPRSYLRQWVYRTPPPVDSGAQ	527
Oy	537	AS 538	
Db	528	SS 529	
RESULT 3			
OTAT13_MOUSE			
ID	OTAT13_MOUSE	PRELIMINARY;	PRT; 529 AA.
AC	Q3TAL13;		
DT	11-OCT-2005,	integrated into UniProtKB/TrEMBL.	
DT	11-OCT-2005,	sequence version 1.	
DT	07-FEB-2006,	entry version 6.	
DE	Activated spleen cDNA, RIKEN full-length enriched library,		
DE	clone:R830012010 product:interleukin 21 receptor, full insert		
DE	sequence.		
GN	Name=I121;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muroidea; Muridae; Murinae; Mus.		
OK	NCBI_taxonomy=1090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NOJ; TISSUE=Activated spleen;		
RC	PUBMED=16141072; DOI=10.1126/science.1112014;		
RA	Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,		
RA	Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,		
RA	Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,		
RA	Davis M.J., Walting L.G., Altieri A., Allen J.E.,		
RA	Abnabel M., Baxter L., Belsel K.W., Bersano T., Bono H., Chaik A.M.,		
RA	Chiu K.P., Choudhury V., Christofides A., Cluttenbuck D.R.,		
RA	Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,		
RA	di Bernardo P., Down T., Engstrom P., Fagiolini M., Faulkner G.,		
RA	Fleischer C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,		
RA	Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,		
RA	Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,		
RA	Hill D., Hummelbeck L., Iacono M., Ieko K., Iwama A., Ishikawa T.,		
RA	Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelsey J., Kilmura H.,		
RA	Kleene H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,		
RA	Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,		
RA	Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,		
RA	Matueda H., Matsuwaga S., Miki H., Mignone F., Miyake S., Morris K.,		
RA	Motagalui-Tabar S., Mulder N., Nakano N., Nakai F., Ng P.,		
RA	Nielsen R., Nishituchi S., Nishikawa S., Noriuchi H., Ohara O.,		
RA	Okazaki Y., Orlando V., Pand K.C., Pavani W.J., Pavese G., Pesole G.,		
RA	Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,		
RA	Roe B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,		
RA	Schönbach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,		
RA	Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,		
RA	Spelling S., Stupka E., Sugtara K., Sultana R., Takemata Y., Taki K.,		
RA	Tamoeia K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,		
RA	Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,		
RA	Yamanishi H., Zdobysky E., Zhu S., Zimmer A., Hide W., Bult C.,		
RA	Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,		
RA	Walstedt C., Metcick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,		
RA	Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,		
RA	Iida Y., Imanura K., Itoh M., Kato T., Kawaji H., Kawagashima N.,		
RA	Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,		
RA	Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,		
RA	Tagami M., Waki K., Wataniki A., Okamura-Ohno Y., Suzuki H., Kawai J.,		
RA	Hayashizaki Y.;		

RT "The transcriptional landscape of the mammalian genome." ;
RL Science 309:1559-1563(2005).
RN
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ND; TISSUE=Activated spleen;
RC MEDLINE=22354683; PubMed=11246851; DOI=10.1038/nature01286;
RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Mikado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogi A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriber L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brat D., Brusic V., Chochia C., Corbani L.E., Cousine S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guentrich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedziński R.M., King B.L.,
RA Konagaya A., Kurtschkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA MacIot D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okado T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wysshaw-Boris A., Yamagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiroki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuda S.,
RA Hara A., Haehizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RT Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs." ;
RL Nature 420:563-573(2002).
RN
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ND; TISSUE=Activated spleen;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Flicsman W., Gaasterland T., Gissi C., King B., Koehwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Mikado I., Pesole G., Quackenbush J.,
RA Schriber L.M., Scandali F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okado T., Furuno M., Aono H., Baldarelli R., Barn G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., De Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guentrich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima U., Mazzerelli J., Mombetere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Togo-Oka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsau S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection." ;
RL Nature 409:685-690(2001).
RN
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ND; TISSUE=Activated spleen;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Suganaka Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Komori H., Akiyama U., Nishi K., Kitsumaki T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwaagi K.,
 RA Fujiwara S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multiplexed capillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RA Atakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Komori H., Murata M., Nakamura M., Nishimura N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 CC -i- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -i- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonCommercial License
 CC -----
 CC EMBL: AK171826; BAE42685.1; -; mRNA.
 DR MGI: MGI:1890475; 1121r.
 DR GO: GO:0003988; F:acylphosphatase activity; RCA.
 DR GO: GO:0004907; F:interleukin receptor activity; IDA.
 DR InterPro: IPR001792; Acylphosphatase.
 DR InterPro: IPR003531; Hemolysate.
 DR PRINTS: PR00112; ACYLPHPTASE.
 DR PROSITE: PS01355; HEMATOPOIETIC_S_FL; UNKNOWN_1.
 DR KEGG: KEGG:01355; HEMATOPOIETIC_S_FL; UNKNOWN_1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 529 AA; 58355 MW; 8841816B0D426581 CRC64;
 Query Match 58.7%; Score 1735.5; DB 2; Length 529;
 Best Local Similarity 62.7%; Pred. No. 2e-115;
 Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;
 QY 1 MPRGMAAPLALLLLGQGWGCPDLYCYTYDTYVTCILEMMNIAHSTLTTLTQDOYEELKD 60
 DB 1 MPRGMAAPLALLLLGQGWGCPDLYCYTYDTYVTCILEMMNIAHSTLTTLTQDOYEELKD 60
 QY 61 EATSCSLHRSANAHATATYTCMDVFFHMADDFSVNTDQSGNYSQSGSFLAESTIKP 120
 DB 61 EATSCSLHRSANAHATATYTCMDVFFHMADDFSVNTDQSGNYSQSGSFLAESTIKP 120
 QY 121 APPNNVTSGGONISRSRDYEDPAFMYLKGKLOEYQYNNRQDPMVAVSRKLISVDS 180
 DB 121 APPNNVTSGGONISRSRDYEDPAFMYLKGKLOEYQYNNRQDPMVAVSRKLISVDS 180
 QY 181 RSVALPLLEFRKDSSEYELQVAGPMPGSSYQGTWSESDPVIPTQSEBELKEGNPHLL 240
 DB 181 RSVALPLLEFRKDSSEYELQVAGPMPGSSYQGTWSESDPVIPTQSEBELKEGNPHLL 240
 QY 241 LLLLVIVIFPAFMSLKTHTPLRLMKKIVA-VSPERFPMPLKYGCGSGDFKXMGAPPTGS 299
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 DB 300 STELGPMSPSPVSTLLEVYSCPPSPAKRDLTELOEAEALVESDGVKPSFWM---PTAQ 356

DB 300 STELVPOSTTTAL-----HLSYPAKEKKFPGILGLEQLECDGMSEPGHWCIIPLAA 354
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 DB 355 GOAVSAYSEEDRRYGLVSDITVTVLDAEGCTTPCSCEDDGYFALDLDALEPSPGLSD 414
 QY 417 PLTAGTTVSCGVASGPGIAGPLSLDRLPLPADGDMAGGLPMGGRSPGVSES 476
 DB 415 LLLVTDPAFLSCGVASGPGIAGPLSLDRLPLPADGDMAGGLPMGGRSPGVSES 474
 QY 477 EAGSPPLAGLMDTRDPSGFGVSDCSSPVCEFTSPGDEGPPRSYLRQWVIPPPLSPQPO 536
 DB 475 EAGSP-PGLMDTRDPSGFGVSDCSSPVCEFTSPGDEGPPRSYLRQWVIPPPLSPQPO 527
 QY 537 AS 538
 DB 528 SS 529
 RESULT 4
 Q3UBS8 MOUSE PRELIMINARY; PRT; 529 AA.
 AC Q3UBS8;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Bone marrow macrophage cDNA, RIKEN full-length enriched library,
 DE clone:1830015L18 product:interleukin 21 receptor, full insert
 DE sequence.
 GN Name=IL21r;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning."
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Bailey T.L.,
 RA Ambesi-Impombato A., Apweiler R., Attalini R.N., Bailei A.M.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
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 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
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 RA Matsuda H., Matuzawa S., Miki H., Mignone F., Miyake S., Moris K.,
 RA Mochizuki-Tabei S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Roost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schombach C., Sekiguchi K., Semple C.A., Seno S., Seiya B., Sheng Y.,
 RA Shibata K., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,

RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide M., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brasic V., Quackenbush J.,
 RA Wahlestedt C., Mattick C., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imanishi K., Itoh M., Kato T., Kawai H., Kawagashita N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tengan M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Quackenbush J.,
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 RA Grimmond S., Guernicchi S., Hirokawa N., Jackson I.J., Jarvis E.D.,
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 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
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 RA Sultana R., Takemura Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
 RA Yuan Z., Zoulan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
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 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kodora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
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 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernicchi S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,

RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hara A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Ogawa K., Tanaka T., Matsura S., Kawai J.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX PubMed=11076861; DOI=10.1101/gr.152600;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Horii F., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Niimiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Saeki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding. (By similarity).
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation. (The box 1 motif is required for JAK interaction and/or
 CC activation. (By similarity)).
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 CC -----
 CC EMBL: AK150824; BAE29886.1; -; mRNA.
 CC MGI: MGI:1890475; 1121x.
 CC GO: GO:0003998; F:acetylphosphatase activity; RCA.
 CC GO: GO:0004907; F:interleukin receptor activity; IDA.
 CC InterPro: IPR001792; Acylphosphatase.
 CC InterPro: IPR003531; Hemip-rcp_S_F1.
 CC PRINTS: PR00112; ACYLPHPTASE.
 CC PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 CC Receptor: Transmembrane.
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 Qy Best Local Similarity 62.7%; Pred. No. 2.3e-115;
 Db Matches 340; Conservative 48; Mismatches 137; Indels 17; Gaps 6;
 Qy 1 MPFGMAFLLLLLLOGGMPDLVYCYDYQYICLEMNLLHPSTLTLMPODYELKD 60
 Db 1 MPFGMAFLLLLLLLHGMSCLDLTCTDYDWTTCVETRRPNSILTMODEYELQD 60
 Qy 61 EATSCSLHRSANNAHTATYTCMDVFPNADIFSVNITDQSGNYGECGSPLLAESIKP 120
 Db 61 QETFCSLHRSCHMTTHIWTTCYCHMRLSQFLSDEVFIVNTDQSGNNGECSPVLAESIKP 120
 Qy 121 APPENVTVTSSGQYNISMRSDYEDPAFYMLKGLQYELQYRNNGDPNAYSPPKRLTSVDS 180
 Db 121 APPLVNTVAFGSGRYSWDSAYDEPSNYVYLRGLQYELQYRNLRNRPVAVPVTKLISVDS 180

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QY 181 RSVSLPLEPRKSSYELQVRAGPMPSGYOGTWSWSDPYIFOTQSEBELKEGNPHLL 240
DB 181 RNVSLPLEEPRKSSYELQVRAGPMPSGYOGTWSWSDPYIFOTQSEBELKEGNPHLL 240
QY 241 LLLLVIFIPAFWMLKTHPLRLMKKIWA--VSPERFPMPLKKGSGDFKMKVGAFTGS 299
DB 241 LLLLVIFIPAFWMLKTHPLRLMKKIWA--VSPERFPMPLKKGSGDFKMKVGAFTGS 299
QY 300 SLELGPMSPVEPSTLEVYSGCHPPSPAKRLQLTLEQPAELVESDGVKPSFW--PTAQ 356
DB 300 SLELGPMSPVEPSTLEVYSGCHPPSPAKRLQLTLEQPAELVESDGVKPSFW--PTAQ 356
QY 357 NSGSAIYSEERDRYGLVSIIDTVYVLDAGBCTPSCSEDGYPALDDAGLESPGLIED 416
DB 357 NSGSAIYSEERDRYGLVSIIDTVYVLDAGBCTPSCSEDGYPALDDAGLESPGLIED 416
QY 417 PLTAGTIVTSGCGVSGSAGSPGLGSLDLRLKPLADGEDMAGLPMGGRSPGVSES 476
DB 417 PLTAGTIVTSGCGVSGSAGSPGLGSLDLRLKPLADGEDMAGLPMGGRSPGVSES 476
QY 477 EAGSPPLAGLMDTDFDSGFGVSDCSSPVACDFTSPGDEGPPRSYLQWVVIPIPLSSPGPQ 536
DB 477 EAGSPPLAGLMDTDFDSGFGVSDCSSPVACDFTSPGDEGPPRSYLQWVVIPIPLSSPGPQ 536
QY 537 AS 538
DB 537 AS 538
QY 528 SS 529
DB 528 SS 529

RESULT 5
QSEBBI_RAT PRELIMINARY; PRT; 521 AA.
AC QSEBBI;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DE 07-FEB-2006, entry version 9.
DE Interleukin 21 receptor (Predicted).
GN Name=IL21r;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alteschul R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: The WSKWS motif appears to be necessary for proper protein

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CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity)
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -----
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC -----
CC EMBL: BC089857.1; -; mRNA.
CC GO: GO:0016021; C: integral to membrane; IEA.
CC GO: GO:0004872; F: receptor activity; IEA.
CC InterPro: IPR003531; Hempr rcpt S Fl.
CC PROSITE: PS01355; HEMATOPOI_REC_S_F1; UNKNOWN_1.
CC Receptor; Transmembrane.
CC SEQUENCE 521 AA; 57439 MW; 37DEF84AE58D755A CRC64;

Query Match 57.6%; Score 1703.5; DB 2; Length 521;
Best Local Similarity 63.3%; Pred. No. 3.7e-113;
Matches 341; Conservative 47; Mismatches 132; Indels 19; Gaps 7;

QY 1 MPRGAAPLLILLIIGGMCBPDVLCYTDYLCIEMKNIHSTLTITQDQYBELKD 60
DB 1 MPRGLAAPLLILLIHGMSCLDLCYTDYLTITCIVLETWSPNPSILSTLTQDVEBELQD 60
QY 61 EATCSLHRSAHNAHTATYTTCMDVFPFMADDIRFVNITDQSGVYSGECSFLLAESTKP 120
DB 61 KETSCSLHAGSHNTTHMYTCMRLSQPMDSDDVFTVNMDDSSNSQDCSFLVAESTKP 120
QY 121 APPNVTVTFSQGYNIISMRSDYEDPAFYMLKGLQYELQYENRSDPMVAISPRKLIYSVS 180
DB 121 APPLNVTVTFSGRIDISMDISTYEEPSNVYLRGKQYELQYENLNLDPAVAVRVTKLISVDS 180
QY 181 RSVSLPLEPRKSSYELQVRAGPMPSGYOGTWSWSDPYIFOTQSEBELKEGNPHLL 240
DB 181 RNISLPLEQFQKSSYELQVRAGPMPSGYOGTWSWSDPYIFOTQSEBELKEGNPHLL 240
QY 241 LLLLVIFIPAFWMLKTHPLRLMKKIWA--VSPERFPMPLKKGSGDFKMKVGAFTGS 299
DB 241 LLLLVIFIPAFWMLKTHPLRLMKKIWA--VSPERFPMPLKKGSGDFKMKVGAFTGS 299
QY 299 LLLLVIFIPAFWMLKTHPLRLMKKIWA--VSPERFPMPLKKGSGDFKMKVGAFTGS 299
DB 299 LLLLVIFIPAFWMLKTHPLRLMKKIWA--VSPERFPMPLKKGSGDFKMKVGAFTGS 299
QY 300 SLELGPMSPVEPSTLEVYSGCHPPSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNSG 359
DB 300 SLELGPMSPVEPSTLEVYSGCHPPSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNSG 359
QY 359 SLELGPMSPVEPSTLEVYSGCHPPSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNSG 359
DB 359 SLELGPMSPVEPSTLEVYSGCHPPSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNSG 359
QY 360 GSAYSEBRDRYGLVSIIDTVYVLDAGBCTPSCSEDGYPALDDAGLESPGLIEDPL 419
DB 360 GSAYSEBRDRYGLVSIIDTVYVLDAGBCTPSCSEDGYPALDDAGLESPGLIEDPL 419
QY 419 GSAYSEBRDRYGLVSIIDTVYVLDAGBCTPSCSEDGYPALDDAGLESPGLIEDPL 419
DB 419 GSAYSEBRDRYGLVSIIDTVYVLDAGBCTPSCSEDGYPALDDAGLESPGLIEDPL 419
QY 420 DAGTTVSGCGVSGSAGSPGLGSLDLRLKPLADGEDMAGLPMGGRSPGVSESTAG 479
DB 420 DAGTTVSGCGVSGSAGSPGLGSLDLRLKPLADGEDMAGLPMGGRSPGVSESTAG 479
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QY 480 SPLAGLMDTDFDSGFGVSDCSSPVACDFTSPGDEGPPRSYLQWVVIPIPLSSPGPQAS 538
DB 480 SPLAGLMDTDFDSGFGVSDCSSPVACDFTSPGDEGPPRSYLQWVVIPIPLSSPGPQAS 538
QY 538 SPLAGLMDTDFDSGFGVSDCSSPVACDFTSPGDEGPPRSYLQWVVIPIPLSSPGPQAS 538
DB 538 SPLAGLMDTDFDSGFGVSDCSSPVACDFTSPGDEGPPRSYLQWVVIPIPLSSPGPQAS 538
QY 539 SP-RGLMDTDFDSGFGVSDCSSPVACDFTSPGDEGPPRSYLQWVVIPIPLSSPGPQAS 539
DB 539 SP-RGLMDTDFDSGFGVSDCSSPVACDFTSPGDEGPPRSYLQWVVIPIPLSSPGPQAS 539

RESULT 6
Q3TA82_MOUSE PRELIMINARY; PRT; 292 AA.
AC Q3TA82;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DE 07-FEB-2006, entry version 5.
DE Activated spleen cDNA, RIKEN full-length enriched library,
clone: F830031M06 product: Interleukin 21 receptor, full insert
sequence. (Fragment).
GN Name=IL21r;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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[1]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=activated spleen;
RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning";
RA Methods Enzymol. 303:19-44(1999).
[2]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=activated spleen;
RA PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells K., Kodius R., Shimokawa K.,
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RA Davis M.P., Wilming L.G., Aidinis V., Allen J.E., Bailey T.L.,
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RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
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RA Schombach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
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RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
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RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
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RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RA "The transcriptional landscape of the mammalian genome";
RA Science 309:1559-1563(2005).
[3]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=activated spleen;
RA PubMed=16141073; DOI=10.1126/science.1112009;
RA RIKEN Genome Exploration Research Group, and Genome Science Group
RA (Genome Network Core Team) and the FANTOM Consortium;
RA "Antisense Transcription in the Mammalian Transcriptome";
RA Science 309:1564-1566(2005).
[4]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=activated spleen;
RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nakazaki T., Osato N., Saito R., Suzuki H., Yamashita I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirml L.M., Kanapin A., Matsumura H., Batilov S., Beisel K.W.,
RA Blake J.A., Bratt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guellinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs";
RA Nature 420:563-573(2002).
[5]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=activated spleen;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamashita I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Offord T., Furuno M., Aono H., Baldarelli R., Barh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guellinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaeets P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schombach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker S., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection";
RA Nature 409:685-690(2001).
[6]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=activated spleen;
RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RA prepare full-length cDNA libraries for rapid discovery of new genes";
RA Genome Res. 10:1617-1630(2000).
[7]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=activated spleen;
RA MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Tanaka K., Tanaka T., Matsuyama S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RA sequencing pipeline with 384 multiplexed sequencer";
RA Genome Res. 10:1757-1771(2000).
[8]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=activated spleen;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watabiki A.,

RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AK172032; BAE42787.1; -; mRNA.
 DR MGI: MGI:1890475; 1121r.
 DR GO: GO:0003998; F:acylphosphatase activity; RCA.
 DR GO: GO:0004907; F:interleukin receptor activity; IDA.
 DR InterPro: IPR003531; Hempt rcpt S Fl.
 DR PROSITE: PS01355; HEMATOPO_REC_S_Fl; UNKNOWN_1.
 DR Receptor.
 KW NON_TER.
 FT SEQUENCE 292 AA; 33609 MW; F071DBC0C2738E33 CRC64;
 SQ
 Query Match 36.6%; Score 1082; DB 2; Length 292;
 Best Local Similarity 67.6%; Pred. No. 4.8e-69;
 Matches 198; Conservative 39; Mismatches 54; Indels 2; Gaps 2;
 QY 1 MPRGMAAPLILLLOGGMGCPDVCYTDYLTQTVICILEMNLHPSTLTTLTQDOYEELKD 60
 DB 1 MPRGPVAAALLLIHGAWSCLDLTCYTDYLTITCVLETRSPNPSILSLTQDOYEELKD 60
 QY 61 EATCSLHRSANHTATYTCMDVPHFMADIFSVNITDQSGNYSQEGCSFLLAESTIKP 120
 DB 61 QETFCSLHRSAGHNTHTIWTYCHMRISQFLSDPEFIVNVTDSGNNSSQEGCSFVLAESTIKP 120
 QY 121 APPPNVTYTFSGQYNISWRSDYEDPAFMYLKGKLYELQYNRQDPMVAVSRKLIISVDS 180
 DB 121 APPLVNVAFFSGRIDISWDASDYDEPSNYLVKGLQYELQYNLRDPVAVRYTLKISVDS 180
 QY 181 RVSALLPLEFRKDSYELQVRAGPMGSSYOGTSEMSDPVIFOTQSEBELKGNPHLL 240
 DB 181 RNVSLPBEFRKDSYQLQVRAAPQGTSTFRGTSEMSDPVIFOTQAGEPRAGMDPHLL 240
 QY 241 LLLLVYVIFPFWSLKTHPLRWLWKKIWA-VSPERFPMPLYKCGSGPKKVV 292
 DB 241 LLAVALIIVL-VFMGLKILHPLRWLWKKIWA-PVTPESFPQPLRHSNGPKKVV 292

RESULT 7
 Q6PEU8_MOUSE PRELIMINARY; PRT; 268 AA.
 AC Q6PEU8;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE 1121r protein.
 GN Name=1121r;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCB1_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueadi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Holik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman V.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Senger A., Schein J.B., Jones S.U.W., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC -----
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 CC -----
 DR EMBL: BC057861; AAH57861.1; -; mRNA.
 DR Ensemble: ENSMUSG00000030745; Mus musculus.
 DR MGI: MGI:1890475; 1121r.
 DR GO: GO:0003998; F:acylphosphatase activity; RCA.
 DR GO: GO:0004907; F:interleukin receptor activity; IDA.
 DR InterPro: IPR003531; Hempt rcpt S Fl.
 DR PROSITE: PS01355; HEMATOPO_REC_S_Fl; 1.
 DR Receptor; Transmembrane.
 KW SEQUENCE 268 AA; 30116 MW; B2EB0C31ACD6DA8 CRC64;
 SQ
 Query Match 29.5%; Score 872; DB 2; Length 268;
 Best Local Similarity 69.6%; Pred. No. 4.5e-54;
 Matches 158; Conservative 30; Mismatches 39; Indels 0; Gaps 0;
 QY 1 MPRGMAAPLILLLOGGMGCPDVCYTDYLTQTVICILEMNLHPSTLTTLTQDOYEELKD 60
 DB 1 MPRGPVAAALLLIHGAWSCLDLTCYTDYLTITCVLETRSPNPSILSLTQDOYEELKD 60
 QY 61 EATCSLHRSANHTATYTCMDVPHFMADIFSVNITDQSGNYSQEGCSFLLAESTIKP 120
 DB 61 QETFCSLHRSAGHNTHTIWTYCHMRISQFLSDPEFIVNVTDSGNNSSQEGCSFVLAESTIKP 120
 QY 121 APPPNVTYTFSGQYNISWRSDYEDPAFMYLKGKLYELQYNRQDPMVAVSRKLIISVDS 180
 DB 121 APPLVNVAFFSGRIDISWDASDYDEPSNYLVKGLQYELQYNLRDPVAVRYTLKISVDS 180
 QY 181 RVSALLPLEFRKDSYELQVRAGPMGSSYOGTSEMSDPVIFOTQ 227
 DB 181 RNVSLPBEFRKDSYQLQVRAAPQGTSTFRGTSEMSDPVIFOTQ 227

RESULT 8
 Q5FA46_CHICK PRELIMINARY; PRT; 590 AA.
 AC Q5FA46;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 21-FEB-2006, entry version 8.
 DE Hypothetical protein.
 GN ORPNames=RCMB04_1b7;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCB1_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Cb; TISSUE=Bursa;
 RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
 RA Fiedler P., Kuter E.S., Blagoderaki A., Koslovskaya D., Kocer M.,
 RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde D.M.,
 RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
 RT genefunction analysis.",

RL Genome Biol. 6:R6-R6(2005).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein (By similarity).
 CC -----
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 CC -----
 DR EMBL, AJ851394; CAH5028.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane, IEA.
 DR InterPro; IPR007110; Ig-like.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Hypothetical protein; Immunoglobulin domain; Repeat; Transmembrane.
 KM SEQUENCE 590 AA; 66332 MW; 369CA086F9A5867 CRC64;
 QY Query Match 25.8%; Score 764; DB 2; Length 590;
 Best Local Similarity 33.0%; Pred. No. 6,56-46;
 Matches 193; Conservative 88; Mismatches 210; Indels 94; Gaps 19;
 Db 12 LLLGGGCGCDLVCTDYDTLVCTVLCILEM-WMLHPSTLTLMQDQYELKDEATSCSLHRS 70
 14 LLEFYSTCHENLCTFVDIVDTLSTCLRNLDGASPYNITATWDE-DDPENTVAACSLLEL 72
 QY 71 AHNATHATYTCMDVFHFMDIFPSVNIITDQSGNYSQECGSLLAESIKPAPPNVTVF 130
 Db 73 SRNANHTEYCTVDMTELDADIRVOVDATELADRHQVHISIGFYMKDNIRPQPFNLAVF 132
 QY 131 SGGYNISWSDYEDPAFYMLKGLQYELQYRNQDPMNAVSRKLISVDSKVSLLPLEF 190
 Db 133 TEGYNIMETHTQNPFLFYLLNGELEQYLRKRRADTWE-TQKISVDEDKETVILPOEF 191
 QY 191 RKXSSVYLQYRAGMPPSSYOGTWSEMDPIVFOGSEBELKE-----GNNPHLLLLLLVI 246
 Db 192 QGNTVEFYQVARRGGTGYGFGEFWSWSSRLTLTSPAAVYQRAQMGW-----MLFFVVA 246
 QY 247 VFIPAFSLKTHPLRLMKKIWAVPSEPFMPLYKGGSGDFKKMGVGAFTGSSLELGPW 306
 Db 247 MVTASTTAFLAKQOSLMKKIACIPDSAFKPKLYLMWNGFKMVGSHMKMTIDLPFW 306
 QY 307 SPEVPSLTLEVYSCPPSPAKRLQLTLEQPAELVESDGVKPSF---WPTAQN--SGG 360
 Db 307 EIVPSEVLEVFMSKPSNCTG-----QEIRLEKNDLPCKPCVSCITLVQDSLLSV 358
 QY 361 SAYSEEDRPYGLVSIPTVTYTLDAEGCTWPCSC-----EDDGYPALDL 404
 Db 359 NSSVTPDRSYGHISITITVYADEFTPCNCCNRMKYKQKNGEDSDAESGYPKXNI 418
 QY 405 -DAGLEPSPGLEDDLDTAGTIVLSGCGVS-----AGSPG-----LGGPLGSLDR-- 448
 Db 419 DDEORRRSSALHSDLSQDKILASGSMSTHLLRTTGAQKQVKGALLEGMSILAEFC 478
 QY 449 LKP-----PLADGE--DMAGC---LPMGGRSPGVSESEKAGSLAGIDMTFD 491
 Db 479 LHPQMDLENPASLPSPDGESVSESGCDFPRRGAR-PGG-----SYMICIDLDPTID 531
 QY 492 SGFVSGDCSSPCEGDFTPSPD-----EGPSPSYLRQWY 524
 Db 532 SGFVSDCGSPVDPEFEONSQTNAESVPLBOEGEDPPRSYVKQNI 576
 RESULT 9
 IL2RB_MACFA
 ID IL2RB_MACFA STANDARD; PRT; 551 AA.
 AC Q38J85;
 DT 10-JAN-2006, integrated into UniProtKB/Swiss-Prot.
 DT 22-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
 DE (High affinity IL-2 receptor beta subunit) (CD122 antigen).
 GN Name=IL2RB;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.

OX NCBI_Taxid=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RA Chen S., Yu L.,
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for interleukin-2. This beta subunit is
 CC involved in receptor mediated endocytosis and transduces the
 CC mitogenic signals of IL2 (By similarity).
 CC -1- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
 CC exists in 3 different forms: a high affinity dimer, an alpha
 CC intermediate affinity monomer (beta chain), and a low affinity
 CC monomer (alpha chain). The high and intermediate affinity forms
 CC also associate with a gamma chain (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein (By similarity).
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intercellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 4
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
 CC -----
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 CC -----
 DR EMBL, DQ223724; AB803908.1; -; mRNA.
 DR PROSITE; PS50853; FN3; 1.
 DR PROSITE; PS01355; HEMATOPOIETIC RECEPTOR SIGNAL; Transmembrane.
 KM Glycoprotein; Membrane; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 26
 FT CHAIN 27 551
 FT FT
 FT TOPO_DOM 27 240
 FT TRANSMEM 241 265
 FT TOPO_DOM 266 551
 FT DOMAIN 131 229
 FT MOTIF 220 224
 FT MOTIF 278 286
 FT CARBOHYD 29 29
 FT CARBOHYD 43 43
 FT CARBOHYD 71 71
 FT CARBOHYD 149 149
 FT DISULFID 36 46
 FT DISULFID 86 86
 SQ SEQUENCE 551 AA; 61224 MW; 5CEAECLA802A1D50 CRC64;
 QY Query Match 9.9%; Score 294; DB 1; Length 551;
 Best Local Similarity 26.4%; Pred. No. 2,4e-12;
 Matches 139; Conservative 73; Mismatches 200; Indels 114; Gaps 30;
 Db 5 WAAPLLILLLLLOGGW-----GCPDLVCTDYDTLVCTVLCILEMWNHPSLTTLTWQDYE 56
 8 WCLPLILLPLLATSSASAAVNGTSRFTCFYNSGRANISCV---WS-----QDG 52
 QY 57 ELKDEATSCSLH---RSANNAI-----HATYTCM-----DVHFEMADIFSVNITD 100
 Db 53 ALQD--TSCGVHAMPDRRRNQCCELLPVSOAMWACLIGTPDSQKLTAVDVTLLKVMC 110
 QY 101 QSGN--YSQEGSFLLAESIKPAPPNVTVF--SCGYNISWSDYEDPAFYMLKGLQY 156
 Db 111 REGVRRMMAIOPKPPENIRLMAPISSLOVYHETHRCNSMKT---SQASHFERLERLF 167
 QY 157 ELOYRNKGDMWAVSPRRKLISVDSRSVSLPLEFRKDSYELOVRAGPMFGSSYQGTWSE 216
 Db 168 EARTLISGHWBAP--LMTLKQKQEWICLETFLPTDQYEFQVRYKPLQGEF--TTWSP 222
 QY 217 WSDPVLVFOGSEBELKEG--WNPILLILLLLLVVLPAPFNSL---KTHPLMLM--KKIN 268
 Db 223 WSPPLAFERRPALGKDTIPMLGLHLVGLSGAGFIIIVLLVLLNCNRTG---WLKKVL 278
 QY 269 A--VSPSEPFMPLVYKGGSGDFKKMGVGAFTGSSLELGPWSVPSPITLVEYSGHPSPSPA 326

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Db      279 KCHTPBPSKFFSQLTSHHGSDVOKMLSSFPSSSFSGGLAPRI-SLELV-----L 328
Qy      327 KRLQTLQLOPAPALVESDGVPKPSFWPTAONSGSAYSEERDRPYGLVSDITVTLDAEG 386
Db      329 ERKVTQL-----LLOQDKVPEPS-----SLSSNRLTSCFTNOGYFFPHLPDALEIHA-- 377
Qy      387 PC-----TW-PCSGEDDGYPALDLDAGLEPSP-----GLEPDLDACTVLSGCCVSAAGSP 437
Db      378 -CQVYFTYDPCAESEEPDEGADAPYTGSSPQPLRLSAED---DAYCTFSGDDLILFFSPS 433
Qy      438 -LGGP-----LGLSLDLRLKPLAD--GEPMAGGLPMGGRSPG 471
Db      434 LGGPSPPTAPGSGSGAGEERLPSLQERVRPM-DQPLGPRTPG 478

RESULT 10
06UAP3_TETNG
ID      06UAP3_TETNG PRELIMINARY; PRT; 512 AA.
AC      06UAP3;
DT      05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT      07-FEB-2006, sequence version 1.
DE      Class I helical cytokine receptor member 13.
GN      Name=CRFAL3;
OS      Tetraodon nigroviridis (Green puffer).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC      Acanthopterygii; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC      Tetraodontidae; Tetraodontidae; Tetraodon.
OX      NCBI_TaxID=99883;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=15496914; DOI=10.1038/nature03025;
RA      Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA      Mancel E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA      Nicaut S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA      Desliva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA      Anthouard V., Jubin C., Castellani V., Kallinka M., Vacherie B.,
RA      Blomont C., Skalli Z., Cattelico L., Poulain J., De Bernardinis V.,
RA      Cuanad C., Duprat S., Broctier P., Couanceau J.-P., Gouzy J.,
RA      Parra G., Lardier G., Chappe C., McKernan K.J., McEwan P., Bosak S.,
RA      Kallia M., Wolf J.-N., Guigo R., Zody M.C., Westrov J.,
RA      Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA      Landier V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA      Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.;
RA      "genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT      the early vertebrate proto-karyotype.";
RL      Nature 431:946-957(2004).
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CC
CC      EMBL: AY374485; AAR25676.1; -. mRNA.
CC      DR      Ensembl: AY374485; Tetraodon nigroviridis.
CC      DR      GO: GO:0004872; F:receptor activity; IEA.
CC      DR      InterPro: IPR003961; FN_III.
CC      DR      Pfam: PF00041; fn3; 1.
CC      DR      PROSITE: PSS0653; FN3; 1.
CC      KM      Receptor.
CC      SQ      SEQUENCE 512 AA; 57191 MW; E058418483A5DF0B CRC64;

Query March 9.7%; Score 286; DB 2; Length 512;
Best Local Similarity 24.4%; Pred. No. 8,1e-12;
Matches 143; Conservative 76; Mismatches 203; Indels 164; Gaps 29;

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Qy      108 ECGSFLAASIKPAPENVTYV-FSGQYNISW-RSDYEDPAFYMLKQLQLEYQYNNRGD 165
Db      111 EESFMALCDVAVKEPASAARVNTTEDSYNTVTHVNVQDLCTIVAR-----VRENRR-- 162
Qy      166 PMAVSRRKLISDSSVSLLPLEFRKSSYELQVRAGMPGSSYOGTWSWSDPV-IFQ 224
Db      163 -MSKEVYSYL-SSDSGHLQIISELLQPRVGYLDVAVAKKCPGLYLGPMSEWSSSAEIRP 220
Qy      225 TQSEELKEGNPHLL-----LILLIVYFIPAFWSLKTPLRMKIKNAVSPERFFMP 279
Db      221 AATSDTAMSW--HLFYTPSVLTLVVVVSLLVSLYLLKNH-----QIPREHFAP 268
Qy      280 LYKSGSGDFPKWVGAPE-----TGSSL-----ELGPMSPVPSLTLEYVSGHPRSPA 326
Db      269 LYHNYGDFKEMVNPVFKCEDYIMTSSQVOMKQEDLLQMSKESSTESKNNKHGHFP 328
Qy      327 KRLQTLQLOPAPALVESDGVPKPSFWPTAONSGSAYSEERDRPYGLVSDITVTLDAE- 385
Db      329 PKLQAO--AHPILLGSDWG-----SQSRGLA-----GPSIHVTLSSEER 368
Qy      386 -----GPTWPCSGEDDGYPALDLDAGLEPSPGLEPDLDACTVLSGCCVSAAGSP 436
Db      369 FEEEGTSQSSACVLRSDODRESFEVEEDWKEQAAGLEB-----AASGLP 414
Qy      437 GLGPGLSLLDLRLKPLADGEDMAAGGLPMGGRSPGVS-----ESEAGSPLAGLMD 488
Db      415 -----PVLQORASSSSGSEDDVPLPHOFFAERKSLDLSLADNQSSEGYR--HYDLD 465
Qy      489 TPDGFGVSDPSPVCEDFTPSGDEGPP-----RSYLROWV 525
Db      466 TIDSGF--GEYNP-----GASPGADQTSLEHINLSNVYKQMW 505

RESULT 11
IL2RB_PANTR
ID      IL2RB_PANTR STANDARD; PRT; 551 AA.
AC      Q38084;
DT      10-JAN-2006, integrated into UniProtKB/Swiss-Prot.
DT      12-NOV-2005, sequence version 1.
DT      07-FEB-2006, entry version 4.
DE      Interleukin-2 receptor beta chain precursor (IL-2 receptor) (p70-75)
DE      (High affinity IL-2 receptor beta subunit) (CD122 antigen).
GN      Name=IL2RB;
OS      Pan troglodytes (Chimpanzee).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC      Pan.
OX      NCBI_TaxID=9598;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [mRNA].
RA      Chen S., Yu L.;
RL      Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Receptor for interleukin-2. This beta subunit is
CC      involved in receptor mediated endocytosis and transduces the
CC      mitogenic signals of IL2 (By similarity).
CC      -1- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
CC      exists in 3 different forms: a high affinity dimer, an
CC      intermediate affinity monomer (beta chain), and a low affinity
CC      monomer (alpha chain). The high and intermediate affinity forms
CC      also associate with a gamma chain (By similarity).
CC      -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC      protein (By similarity).
CC      -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC      folding and thereby efficient intracellular transport and cell-
CC      surface receptor binding (By similarity).
CC      -1- DOMAIN: The box I motif is required for JAK interaction and/or
CC      activation (By similarity).
CC      -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 4
CC      subfamily.
CC      -1- SIMILARITY: Contains 1 fibronectin type-III domain.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms

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CC EMBL: DQ23725; ABB03909.1; -- mRNA.

DR PROSITE; PS50853; FN3, 1.

DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.

KW Glycoprotein; Membrane; Receptor; Signal; Transmembrane.

FT SIGNAL 1 26 By similarity.

FT CHAIN 27 551 Interleukin-2 receptor beta chain.

FT /Ftrd=PRO 0000045410.

FT TOPO_DOM 27 240 Extracellular (Potential).

FT TRANSHEM 241 265 Potential.

FT TOPO_DOM 266 551 Cytoplasmic (Potential).

FT DOMAIN 131 229 Fibronectin type-III.

FT MOTIF 220 224 WSXS motif.

FT MOTIF 278 286 Box 1 motif.

FT CARBOHYD 29 29 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 43 43 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 71 71 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 149 149 N-linked (GlcNAc. . .) (Potential).

FT DISULFID 36 46 By similarity.

FT DISULFID 74 86 By similarity.

FT SEQUENCE 551 AA; 61126 MW; 5C4B1ECB17BEF52B CRC64;

Query Match 9.5%; Score 280; DB 1; Length 551;

Best Local Similarity 25.6%; Pred. No. 2,4e-11;

Matches 134; Conservative 76; Mismatches 204; Indels 110; Gaps 30;

QY 5 WAAPLLLLL-LOGG-----GCPDLVCTYDLYQYICLEMNHLHPSTLTITWQOYE 56

DB 8 WRPLPLLLPLAPWASATVNGTSOPTFYNSRANISCV-----WS-----QDG 52

QY 57 ELDEATSGSLH-----RSANNA-----HATVCHM-----DVHFMAADIFSNITD 100

DB 53 ALQD--TSCOVHAMPDRRNQTELLPVQSASACNLIIGAPSOGLTYDITLKLVC 110

QY 101 QSGNYSOECG--SFLLAESIKPAPFNVTVTF--SGQYNISWSDYEDPAFYMLKGLQY 156

DB 111 REGVWRVMAIQDKPENRLMAPISLQVHVHETHCNISMEI---SQASHYERHLEF 167

QY 157 ELQYRNQDWMANSPRKLISVDSRSVSLPLERKSSSYELQYRAGPMSSYQGTWSE 216

DB 168 EARTLSFGHTWBEAP--LTLTKQKQKOWICLETLPPTQYEFQVRYKPLQGEF--TTWSP 222

QY 217 WSPVIRFQTOSEBEKEG--WNPHLLLLLVLVIFPAFMSL-----KTHPMLRLM-KKIW 268

DB 223 WSOPLAFRIKPAISGKOTTPMLGHLVGLSCAFPIILVILINCRNTGP---WLKKVL 278

QY 269 A--VPSPERFEMPLYKCGSGDFKKMGVAPFTGSSLELGPMSPVPSLTLEVYSCHPRSSPA 326

DB 279 KCHTPDSKFFSQSLSEHGQVQKWLSPFSSSFSGGLAPEI-SPLEV-----L 328

QY 327 KRLQLETPALQEPALVESDGYPKPSEFWPTAQNSSGASVSEEDRYGLVSDITVVLDAEG 386

DB 329 ERDKVITL-----LLOQDKVPEPA-----SLSSNHSILTSCFNTQGYFFPHLPDALEIEA-- 377

QY 387 PC-----TWPCSCEDD-----GYPALDLADGLEPSPGLD-----PLLDAGTVLSCGCV 431

DB 378 -COVYFTYDYAEEDADEGVAAGAPRTGSSPOPLQSLGEDDYCTFPSPRD-GLLIFPSLL 435

QY 432 SAGSPGLGPIGLSL--DRLKPLAD--GEDWAGLPMGGRSPG 471

DB 436 CGSPSPSTAPGSGAGGERMPSPSQGERVPRMW-DPQPLGPTPG 478

RESULT 12

IL2RB HUMAN STANDARD; PRT; 551 AA.

AC PI4784;

DT 01-APR-1990, integrated into UniProtKB/Swiss-Prot.

DT 01-APR-1990, sequence version 1.

DT 07-MAR-2006, entry version 78.

DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75) (p75) (High affinity IL-2 receptor beta subunit) (CD122 antigen).

GN Name=IL2RB;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RX MEDLINE=89242117; PubMed=2785715;

RA Hakeyama M., Tendo M., Minamoto S., Kono T., Doi T., Miyata T.,

RA Miyasaka M., Taniguchi T.,

RT "Interleukin-2 receptor beta chain gene: generation of three receptor

RT forms by cloned human alpha and beta chain cDNA's,"

RL Science 244:551-556(1989).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RX PubMed=15461802; DOI=10.1186/gb-2004-5-10-r84;

RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.,

RA Cole C.G., Goward M.E., Aguado B., Maliya M., Mokrab Y., Huckle E.J.,

RA Beare D.M., Dunham I.,

RT "A genome annotation-driven approach to cloning the human ORFeome,"

RL Genome Biol. 5:RESEARCH84.1-RESEARCH84.11(2004).

RN [3]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RA Rieder M.J., Amel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,

RA Rajkumar N., Toth B.J., Yi Q., Nickerson D.A.;

RT "SeatleSNPs, NHLBI H66682 program for genomic applications, UW-

RT FHRCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>)";

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/9900311;

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,

RA Clamp M., Smink L.J., Alincough R., Almeida J.P., Babbage A.K.,

RA Bagnoley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

RA Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,

RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,

RA Conroy D., Corby N.R., Coxville G.J., Cox A.V., Davis J., Dawson E.,

RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,

RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,

RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,

RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

RA McLaren I.D., Mashreghi-Mohammadi M., Matthews L.H., McEwen O.T.,

RA McElay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,

RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.C.T.,

RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,

RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers S., Shimizu N.,

RA Minooshima S., Kawasaki K., Sasaki T., Asakawa S., Kodoh Y.,

RA Shirohani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuana S.,

RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,

RA Lewis J., Lewis S., Lin S.-P., Lon P., Malaj E., Nguyen T., Pan H.,

RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,

RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,

RA Zhan M., Zhang G., Chisose S., Murray J., Miller N., Mink P.,

RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,

RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,

RA Hinds K., Kemp K., Lareille P., Layman D., Ozerky P., Rohlfing T.,

RA Scheet P., Walker C., Wamley A., Wohlmann P., Pepin K., Nelson J.,

RA Korf I., Bebeli J.A., Hillier L.M., Mardis E., Waterston R.,

RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,

RA Badar M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,

RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanecki J.P.,

RA Peyrard M., Kedra D., Serousi E., Fransson I., Tapia I., Bruder C.E.,

RA O'Brien K.P., Wilkerson P., Bodentelch A., Hartman K., Hu X.,

RA Khan A.S., Lane L., Tlahun Y., Wright H.;

RT "The DNA sequence of human chromosome 22." ;
 RL Nature 402:469-495(1999).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lung;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.F., Schuler G.D.,
 RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.P., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.J.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullan S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Vallat D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pheby J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield A.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP 3D-STRUCTURE MODELING OF 31-230.
 RX MEDLINE=9511955; PubMed=7529123;
 RA Bamboatrough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 modelling." ;
 RL Structure 2:839-851(1994).
 CC -1- FUNCTION: Receptor for interleukin-2. This beta subunit is
 involved in receptor mediated endocytosis and transduces the
 mitogenic signals of IL2.
 CC -1- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
 exists in 3 different forms: a high affinity dimer, an
 intermediate affinity monomer (beta chain), and a low affinity
 monomer (alpha chain). The high and intermediate affinity forms
 also associate with a gamma chain.
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 protein.
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 folding and thereby efficient intracellular transport and cell-
 surface receptor binding.
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 activation.
 CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 4
 subfamily.
 CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
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 CC -----
 DR EMBL: M26062; AAA59143.1; -; mRNA.
 DR EMBL: CR456506; CAG30392.1; -; mRNA.
 DR EMBL: AF517934; AAM54040.1; -; Genomic DNA.
 DR EMBL: AL022314; CA18444.1; -; Genomic DNA.
 DR EMBL: BC025691; AAH25691.1; -; mRNA.
 DR FIR: A30342; A30342.
 DR PDB: 1ILM; Model; B=31-230.
 DR PDB: 1ILN; Model; B=31-230.
 DR PDB: 2BS1; X-ray; B=27-240.
 DR Ensembl: ENSG00000100385; Homo sapiens.
 DR H-InvDB: HIX0016437; -.
 DR HGNC: HGNC:6009; IL2RB.
 DR MIM: 146710; gene.
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.
 DR GO: GO:0005886; C:plasma membrane; TAS.
 DR GO: GO:0004911; F:interleukin-2 receptor activity; TAS.
 DR GO: GO:0006461; P:protein complex assembly; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.

DR InterPro: IPR002996; Cytok_rcpt_B/G.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hempe_rcpt_S_F1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS50853; FN3; 1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
 KW 3D-structure; Glycoprotein; Membrane; Polymorphism; Receptor; Signal;
 Transmembrane.
 FT SIGNAL 1 26
 FT CHAIN 27 551
 FT
 FT TOPO_DOM 27 240
 FT TRANSMEM 241 265
 FT TOPO_DOM 266 551
 FT DOMAIN 131 229
 FT MOTIF 220 224
 FT MOTIF 278 286
 FT CARBOHYD 29 29
 FT CARBOHYD 43 43
 FT CARBOHYD 71 71
 FT CARBOHYD 149 149
 FT DISULFID 36 46
 FT DISULFID 74 86
 FT VARIANT 83 83
 FT VARIANT 83 83
 FT VARIANT 391 391
 FT STRAND 35 37
 FT STRAND 39 43
 FT STRAND 45 47
 FT STRAND 51 57
 FT STRAND 60 64
 FT STRAND 66 67
 FT STRAND 68 70
 FT STRAND 72 73
 FT STRAND 75 76
 FT TURN 80 82
 FT STRAND 85 86
 FT TURN 90 92
 FT HELIX 93 95
 FT STRAND 96 104
 FT STRAND 106 109
 FT STRAND 112 116
 FT STRAND 118 122
 FT STRAND 132 133
 FT STRAND 138 138
 FT HELIX 139 142
 Query Match 9.4%; Score 278; DB 1; Length 551;
 Best Local Similarity 26.0%; Pred. No. 3.3e-11;
 Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;
 QY 5 MAAPLILLL--LGGW-----GCPDLVCYTDVLYQYICLLEMMNHLPTLTLTWQOYE 56
 DB 8 WRLEPLILLLPLPLATSWASAAVNGTSQTCFYNSRANISCV--WS-----ODG 52
 QY 57 ELKDEATSCSIH---RSANAT-----HATVTCM-----DVFHMAADIFSVNITD 100
 DB 53 ALQD--TSCQVHAMPRDRNQCCELLPVSQAAGACNLIGAPDSOKLTVVDITLRLVLC 110
 QY 101 QSGNYSOECG--SEFLAESTKPAAPFNVYTF--SGQYINISMSDVEDPAPFMYLKGKLYQ 156
 DB 111 REGVWRVMAIODFKPENRLMAPISLQVHVHETHRCNISWEI--SQASHYFERHLEF 167
 QY 157 ELQRRNGDPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQVRAGPMGSSSYQGTWSE 216
 DB 168 EARTLSPGHTWEAP--LITLKQKQEWICLETLPDTPQYEFQVRVAPLQGER--TWSP 222
 QY 217 WSDPVIFQTOSEBIKEG--WNPHLLLLLVIVFIPAFNSL-----KTHPLMLRLW-KKIW 268
 DB 223 WSGPLARTRPALKQDTIWMGLHLVLGSGARGFILLVYLLINCRVTGP---WLKXVL 278
 QY 269 A--VPSERFRFMPLYKCGSDPFKKWGVAPFTGSSLELGPMSPEVPSLTLEYVSCHPRPSA 326

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Db      279 KCMFPDPSKFFSGLSSSEHGQVQKMLSPFSSSSPGLAPEI-SPELV-----L 328
Qy      327 KRLOLTQELQPAELVESDGVKPSFWPTAQNSSGANSSEEDRPGLVSDITVTVLDAEG 386
Db      329 ERDKVETOL-----LLQDKVPEPA-----SLSSNHSILTSCFTNOGYFFPHLLDALEIEA-- 377
Qy      387 PC-----TWPSCCED-----GYPALDLDALEPSPGLEPDLDACTVTLSCGCVASGSP 436
Db      378 -CQVYFTIDYSEEDPDEGVAAGAPLGSSPQLPLSG-ED---DAYCTFPRDILLFSP 432
Qy      437 G-LGPF-----LGLSLDLRLKPLAD--GEDMAGGLPWGGRSPG 471
Db      433 SLGGPSPPTAPGSSGAGEERMPSLQERVRDWM-DPQLGPRTPG 478

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RESULT 13
Q2VB08 BRARE PRELIMINARY; PRT; 509 AA.
AC 02VB08;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE Erythropoietin receptor.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bahtary N., Caro J., Handin R., Zon L.,
RT "Functional conservation of epo-epror signaling in zebrafish.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: DO273166; AB877800.1; -; mRNA.
KW GO: GO:0004872; F:receptor activity; IEA.
KW Membrane; Receptor; Repeat; Transmembrane.
SQ SEQUENCE 509 AA; 57872 MW; ADA014E174FCD380 CRC64;

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Query Match      8.8%; Score 261; DB 2; Length 509;
Best Local Similarity 26.5%; Pred. No. 4.9e-10;
Matches 130; Conservative 70; Mismatches 204; Indels 86; Gaps 25;

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Qy      22 DLVCYTDYLTQVLCILEN--WNLHPSTLTLTWDDQVELKDEATSGSLHRSANHTAT 78
Db      41 DIKCFVGGKQDFTCFWEKEDGTNSODNYFTFYTMENKMDCAVS-SLFLSSN-RSV 97
Qy      79 YTCNM-DVFHFMADDISVNTTDSQNSQSCSFLAESTIKRPPFNVTYTFG---GQY 134
Db      98 FPCPLPALFTSLDVOVLRDQMLYKNSLVNENILLTD---PPRVTYWSGKGGQL 152
Qy      135 NISWRSDYEDPAFALMKGLQYELQYRNKDPMAVSPRKLISVDSRSVLLPLE-PRKD 193
Db      153 NVSWL-----PPAVKYIDSLIYEVY-----AVESHMCKVETKASTMLVLRGLQPD 201
Qy      194 SSVELQVRAGMPGSSYQGTWSEWSDPYTFOTGSEELKEGNNPLLILLIIVIFIPAFW 253
Db      202 TRYKVMVRVKR-DEVSYKGYWSSWTSPVIAVT-----PPGSMDDLIVLVLVFIILLCL 255
Qy      254 S-----LTHPLMLRMKKTIWA-VPSRPFPMFLYKCGSGDPFKWVGAPRTGS-----SLIEG 304
Db      256 SMVTYLSHHKR--LLKKLMPDIPTEHKFPGLFTVYKGFKEWM-SQNSGSMWARSVQM- 311
Qy      305 PMSPEVSTLEVYSCHPSPRPAKRLQTLQELQPAELVESD-----GYPKPSPFNPTAQN 359

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Db      312 -YTEELSPLEVL-----EVSLSPLDERKLVREDDQSDSLTEPRHMLMEQLRA 361
Qy      360 GSATSEERDRPYGLVSDT-VTVLDAEGPCTWCSCEDDGYPALDLDALEPSPGLEPDL 418
Db      362 LQENPESLSSTLLQSDHYITLHSSGG-----QREDDVF-----ETLPLDTLF 407
Qy      419 LDAGTVLSCGCVASGAPGLGSLDLRLKPLADGEDMAGGLPWGGRSPGCVSSSEA 478
Db      408 TSAQTSINNSHDLGLSLRQSASGRLSQ-----SSFED--PNHPMPRPGVAYMAVA 460
Qy      479 GSPLAGLMD 488
Db      461 DS---GVSLD 467

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RESULT 14
Q9Z1A0_CAVPO PRELIMINARY; PRT; 890 AA.
AC Q9Z1A0;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Interleukin-5 receptor beta chain.
GN Name=IL5;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Logsdon N.J., Graham A., Scott C.W.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR HSSP: U94688; AAC77520.1; -; mRNA.
DR HSSP: P32927; IGH7.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004907; F:interleukin receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0019221; P:cytokine and chemokine mediated signaling p. .; IEA.
DR InterPro: IPR002996; Cytok rcpt_B/G.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003531; Hempc_rcpt_S_PL.
DR InterPro: IPR011365; IL3_rcpt_beta.
DR Pfam: PF00041; fn3_3.
DR PIRSF: PIRSF001956; IL3R_beta_c_1.
DR SMART: SM00060; FN3_3.
DR PROSITE: PSS0853; FN3_3.
DR PROSITE: PS01355; HEMATOPO_REC_S_PL; UNKNOWN 1.
KW Membrane; Receptor; Transmembrane.
SQ SEQUENCE 890 AA; 96579 MW; D43FB1CA8852536 CRC64;

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Query Match      8.5%; Score 250; DB 2; Length 890;
Best Local Similarity 22.7%; Pred. No. 6.2e-09;
Matches 150; Conservative 73; Mismatches 217; Indels 220; Gaps 36;

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Qy      2 PRGMAPLLLLLIQGGGCP-DLVCTDYLTQVLCILEMNNLHPSTLTLM----- 51
Db      229 PSQWSPVSVSSQPGQAGQNLQCVFDAGHTLSCGMEVRSQVTSVSGFLFYRSSLDAG 288
Qy      52 -----QDQVELKDEAT--SCSLHRSANHTATATYTCMDVDFHFMADDFSVNITDQSG- 103
Db      289 EQRCPQVQKELHDIDYTRHSCQI-RVSNPRPHSQYT-----VTVPRNGE 332

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QY 104 NYSOEGSFLAESTIKPAPPNVTVTFSGOYINISWRSDDYEDPAPFYLKGLQYELQYRNR 163
DB 333 KFIISANHIQWA-----APFLNVTKD-GDYISLHWYTE---KNYHSIENTFEIQYRTA 382
QY 164 GDPWAVSPRRKLISVDSRSVSLPLFEFRKDSYELQYRAGPMPSYQGTWSEMSDVIF 223
DB 383 GDRRENSKTEFL-KNANHNPFLPPLF-PATTVIARVVKSPCGAANGIMSEMSBQRW 438
QY 224 QTOSEELKEGNN-PHILLILLIVFIP-----AFMSLKHPLMLRKWKIWAIVSPERFF 277
DB 439 TTD-----WALPTWIALVLVITLALLALRFCGLYGYRLRKXKE--KINPSPKSH 489
QY 278 M-----PLKGGSGDFKKWVG-APFTSSLELQWSPSEVSTL 314
DB 490 LFKNGSAGRLPDSRMAPASRSAPSWGWSGRFLFICVCPADSRDESVSLTTEDPYIV 549
QY 315 EYVSHCHPPSPAKLQLTQELQPAELVESDVPKPSFWPTQNSGSAVSEDRPYGLV 374
DB 550 -----CDPPEPHSPASDLQEQPSPVQPPVP-----QDQPG--- 585
QY 375 SIDTVVLDAEGPCTWP-----CSCEDDG-----YPALDLD 405
DB 586 --DQLATFDFENGPLYGRPHSHSLPDLAQGQPKPELPGSLLEYLCLPGGSAQLVPLAQAT 643
QY 406 AGLEPSFGLDPLDAGTIVLSC--GCYSAGSPGL---GGPLGSLDLRLKPLADGEDWA 460
DB 644 GQAQPAFG-----ECLSGPYTQSPYLEAGGGP-----APPASDPGSA 682
QY 461 GGLPWGGRSPG---VSESEAGSPLAGMDPTFSGFV-----GSDCS-----P 502
DB 683 QG---PDGGRDSDVILPTNSGP-----EHPVASGVYTTADLTLTSTASSVSLAPPP 735
QY 503 VECDFTS-----PGDEGP-PRSYLRQWVIPP---PLSSPG-PQ 536
DB 736 DLCPGLSDEAPAPPTPKRPFEGYVELPASWGPPLPKSFLGQFV--PPAPSSPVLSGPHQ 793

RESULT 15
IL2RB RAT STANDARD; PRT; 537 AA.
ID IL2RB RAT
AC P26896;
DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1992, sequence version 1.
DT 07-MAR-2006, entry version 51.
DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
DE Interleukin-2 receptor beta chain subunit (CD122 antigen).
DE (High affinity IL-2 receptor beta subunit) (CD122 antigen).
GN Name=IL2rb;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RX MEDLINE=91364784; PubMed=1889461;
RA Page T.H., Dailman M.U.;
RT "Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha
RT and beta chain genes: differentially regulated gene activity in
RT response to mitogenic stimulation.";
RL Eur. J. Immunol. 21:2133-2138(1991).
CC -1- FUNCTION: Receptor for interleukin-2. This beta subunit is
CC involved in receptor mediated endocytosis and transduces the
CC mitogenic signals of IL2.
CC -1- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
CC exists in 3 different forms: a high affinity dimer, an
CC intermediate affinity monomer (beta chain), and a low affinity
CC monomer (alpha chain). The high and intermediate affinity forms
CC also associate with a gamma chain.
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
```

```
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 4
CC subfamily.
CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial License
CC -----
DB EMBL; M55050; AAA41429.1; -, mRNA.
DB HSBP; P14784; IILM.
DB RGD; 2896; 112rd.
DB InterPro; IPR002996; Cytln rcpt_B/G.
DB InterPro; IPR003961; FN_III.
DB InterPro; IPR003531; Hmpt_rcpt_S_F1.
DB PROSITE; PS50853; FN3; 1.
DB PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
DB Glycoprotein; Membrane; Receptor; Signal; Transmembrane.
DB SIGNAL 1 26
DB CHAIN 27 537
DB TOPO_DOM 27 239
DB TRANSMEM 240 267
DB TOPO_DOM 268 537
DB DOMAIN 132 230
DB MOTIF 221 225
DB MOTIF 280 288
DB CARBOHYD 43 43
DB CARBOHYD 55 55
DB CARBOHYD 71 71
DB CARBOHYD 150 150
DB DISULFID 36 46
DB FT DISULFID 74 86
DB FT SEQUENCE 537 AA; 60657 MW; 9C744A24F361968 CRC64;

Query Match 8.4%; Score 248; DB 1; Length 537;
Best Local Similarity 23.6%; Pred. No. 4.5e-09;
Matches 148; Conservative 70; Mismatches 178; Indels 232; Gaps 33;

QY 5 WAAFL-LILLLOGW-----GCPDLYCYDYLVQVLCILEMKNLHPSTLTLTWQOYE 56
DB 8 WRPLPLYILLILLATTWWSAAVNDCHLKFYNSRANVC--MWS----- 49
QY 57 ELKDEA---TSCSILHRAH---NAT-----HATTCHM-----DVFHMADDI FSV 96
DB 50 --PEEALNVTISCHTHAKSDRMHMKTELTLPVRQASWACNLILGRLPDQSGLTSVDLST 107
QY 97 NIT--DQSGNYSOEGSFLAESTIKPAPPNVTVTF--SGOYNISWR-----SDYEDPAFY 148
DB 108 SVVCWESEKGRKRVYCTTFHPEDNRLAPHSLOYLHETRCNISWEVSQVSHVNP--- 164
QY 149 MLKGLQYELQYRNGDPMWAVSPRRKLISVDSRSVSLPLFEFRK-----DSSYEL 198
DB 165 -----YLEFE-----ARRRLDRSWEDEASVFSLKQROQWFLFETLPTDTSYEL 207
QY 199 QVRAQPMPSGYQGTSEMSWSDPVYFQOSEELKEGNNPHILLILLIVFIPAPWS--- 254
DB 208 QVRVIAQRGKTI--RTWSPMSQPMAFRRPADPKCIFPLMRLCLLLVLGCEFGGLSCVCV 265
QY 255 -----LKHPLMLRKWKIWAIVSPERFFMPPLYKGGSGDFKKWVAPF--- 296
DB 266 LVKCRYIGPMUKTLKLKH-----IPDSSEFSSQLSSQHGDLQKTLSSPVQSF 314
QY 297 --TGSSLELQWSPSEVSTLEVYSCHPPSPAKRLQLTQELQPAELVESDGVKPSFWP 353
DB 315 FSPFGSAPEISP-----LEVLD-----RDSKTQMMLFQK-----EKASSPS- 352
QY 354 TAQNSGSAVSEEDRPY-----GLVSDTVVLDAEGCTWPCSCEDDGYPLDLDAG 407
DB 353 -----SGHSQASCFPNQGYFFFHLSNLALEISSCOYFTFYDCMBE-DVEEDG-PRLPESP 406
QY 408 LEP-----SPGLEDPILLDAGTIVLSCGCVSAGSPGLGGLP-----GSLDLRLK 450
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Db      407 LPPLPFTGEODDYCAFPDDLL-----FSPSMSTPNTAYGNSITPEER 452
QY      451 PPLADGEDWAGLPMGGRSPGVSESEBAGSPLAGIDMDTFDSCFVGSDDCSSPVECDFTSP 510
Db      453 PPLSLQE---GLP-----SLASPDLMGL-----QHPLELEL--- 480
QY      511 GDEGPPRSYLRQWVVIPPPSSPGPOAS 538
Db      481 GDDEGMS-----TNSGQOAS 497
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Search completed: September 7, 2006, 12:51:27
Job time : 300.669 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:51:46; Search time 53.8 Seconds
(without alignments)
875.306 Million cell updates/sec

Title: US-10-659-684-115

Perfect score: 2958
Sequence: 1 MPRGMAAPLLLLLLQGSGMGC.....YLQGWVVPPLSPGPGAS 538

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/iaa/5.COMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/iaa/6.COMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/iaa/7.COMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/iaa/H.COMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCUS.COMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/iaa/RE.COMB.pep:*
- 7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2958	100.0	538	2	US-09-040-005-2
2	2958	100.0	538	2	US-09-522-217-115
3	2958	100.0	538	2	US-09-404-641-2
4	2958	100.0	538	2	US-09-923-246-115
5	2958	100.0	538	2	US-10-295-723-115
6	2958	100.0	538	2	US-10-414-186-2
7	2958	100.0	538	2	US-09-825-561A-2
8	2958	100.0	538	2	US-10-243-072-2
9	2958	100.0	538	2	US-10-282-622-16
10	2958	100.0	547	2	US-09-949-016-11544
11	2817	95.2	568	2	US-09-825-561A-65
12	1735.5	58.7	529	2	US-09-404-641-85
13	1735.5	58.7	529	2	US-10-414-186-85
14	1735.5	58.7	529	2	US-09-825-561A-12
15	1735.5	58.7	529	2	US-10-243-072-85
16	1729.5	58.5	529	2	US-09-784-859-6
17	1729.5	58.5	529	2	US-09-784-859-6
18	1302	44.0	567	2	US-09-825-561A-16
19	1221.5	41.3	397	2	US-09-404-641-81
20	1221.5	41.3	397	2	US-10-414-186-81
21	1221.5	41.3	397	2	US-10-243-072-81
22	1197	40.5	606	2	US-09-522-217-97
23	1197	40.5	606	2	US-09-404-641-51
24	1197	40.5	606	2	US-09-923-246-97
25	1197	40.5	606	2	US-10-295-723-97
26	1197	40.5	606	2	US-10-414-186-51

27	1197	40.5	606	2	US-09-825-561A-30	Sequence 30, Appl
28	1197	40.5	606	2	US-10-243-072-51	Sequence 51, Appl
29	1195	40.4	218	2	US-09-825-561A-6	Sequence 6, Appl
30	1135	38.4	261	2	US-09-825-561A-71	Sequence 71, Appl
31	1100	37.2	247	2	US-09-825-561A-69	Sequence 69, Appl
32	844	28.5	486	2	US-09-825-561A-73	Sequence 73, Appl
33	677.5	22.9	240	2	US-09-404-641-70	Sequence 70, Appl
34	677.5	22.9	240	2	US-10-414-186-70	Sequence 70, Appl
35	677.5	22.9	240	2	US-10-243-072-70	Sequence 70, Appl
36	278	9.4	551	2	US-09-194-145-2	Sequence 2, Appl
37	278	9.4	551	2	US-09-949-002-308	Sequence 308, App
38	278	9.4	551	7	549756-2	Patent No. 549756
39	278	9.4	551	7	549756-2	Patent No. 549756
40	278	9.4	594	2	US-09-949-002-537	Sequence 537, App
41	248.5	8.4	539	7	549756-4	Patent No. 549756
42	247.5	8.4	539	7	5198359-4	Patent No. 5198359
43	231	7.8	536	2	US-09-949-016-8560	Sequence 8560, Ap
44	220.5	7.5	468	1	US-08-164-614A-7	Sequence 7, Appl
45	220.5	7.5	468	1	US-08-456-489B-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-040-005-2
Sequence 2, Application US/09040005
Patent No. 6057128

GENERAL INFORMATION:

APPLICANT: Donaldson, Debra

TITLE OF INVENTION: MU-1 RECEPTOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESS: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/040, 005

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G15320

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-498-8224

TELEFAX: 617-876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 538 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-040-005-2

Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3 6e-267; Indels 0; Gaps 0;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLQGSGMGCPCDVCYTDYICILEMNLAPSTLTLTWQDYEEIKD 60
DB 1 MPRGMAAPLLLLLLQGSGMGCPCDVCYTDYICILEMNLAPSTLTLTWQDYEEIKD 60

QY	6	EATSCSLRSRANNAHATYTCCHMDVHPMAADDIFSNIITDOSGNSYOEGCSFLAASIKR	120
Db	61	EATSCSLRSRANNAHATYTCCHMDVHPMAADDIFSNIITDOSGNSYOEGCSFLAASIKR	120
QY	121	APPFNVTYTFSGQYNIWSRSDYEDPAFYMLKGLQYELQYLRNKGDMAVSPRKLISYDS	180
Db	121	APPFNVTYTFSGQYNIWSRSDYEDPAFYMLKGLQYELQYLRNKGDMAVSPRKLISYDS	180
QY	181	RSVSLLPLEFRDSSYLEQVRAQPMFGSSYQGTWSSWSPVYFQTOSEELKEGWNHLL	240
Db	181	RSVSLLPLEFRDSSYLEQVRAQPMFGSSYQGTWSSWSPVYFQTOSEELKEGWNHLL	240
QY	241	LLLLIVYIIPAFWSLKTHERLMLRMKKIYAVPSPERFEMFLYKGCSDGFKKMGAPETGSS	300
Db	241	LLLLIVYIIPAFWSLKTHERLMLRMKKIYAVPSPERFEMFLYKGCSDGFKKMGAPETGSS	300
QY	301	LELGWSPSEVPSTLEVYSGHPSPSPAKRIQTELQEPALVSDGYPKOSFWPFTAQNSGG	360
Db	301	LELGWSPSEVPSTLEVYSGHPSPSPAKRIQTELQEPALVSDGYPKOSFWPFTAQNSGG	360
QY	361	SAYSEERPRPGLVSIIDYTVLDAESPCTWPCSCBEDGYPALDLNGLBSPSLBEPPLD	420
Db	361	SAYSEERPRPGLVSIIDYTVLDAESPCTWPCSCBEDGYPALDLNGLBSPSLBEPPLD	420
QY	421	AGTYTLCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGGLPMWGRSPGVYSEBAGS	480
Db	421	AGTYTLCGCVSAGSPGLGGLGSLDLRLKPLADGEDWAGGLPMWGRSPGVYSEBAGS	480
QY	481	PLAGIDMTPTPSGPFVSGDCSSPVECDTSPGDEGPRSLTRQWVYTPPLSLSPGQAS	538
Db	481	PLAGIDMTPTPSGPFVSGDCSSPVECDTSPGDEGPRSLTRQWVYTPPLSLSPGQAS	538

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RESULT 2
US-09-522-217-115
Sequence 115 Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Preenell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-09-522-217-115

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Query Match	100.0%;	Score 2958;	DB 2;	Length 538;
Best Local Similarity	100.0%;	Pred. No. 3.6e-267;		
Matches 538;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Oy 1 MPRGAAPLLLLLLGGMGCRDVCYTYDYLQTVICILEMNNLHPSLTTLTWODQYBELKD 600
    |||||
Db 1 MPRGAAPLLLLLLGGMGCRDVCYTYDYLQTVICILEMNNLHPSLTTLTWODQYBELKD 600

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Oy	6	EATSGSLHSSAHNAHTAATYTCMDVDFHHMADIDFSVNTIDDSGNYSGECSFLLAEBIKP	1.30
Db	61	EATSGSLHSSAHNAHTAATYTCMDVDFHHMADIDFSVNTIDDSGNYSGECSFLLAEBIKP	1.20
Oy	121	APPFNVTYFSGQYINISMRSDYEDBAPYMLKGKLYELQYLRNKGDPMAVSPRRKLISVD	1.80
Db	121	APPFNVTYFSGQYINISMRSDYEDBAPYMLKGKLYELQYLRNKGDPMAVSPRRKLISVD	1.80
Oy	181	RSVSLLPLEFRDSSYELOVRAGPMPGSSYOGTWSBMSDPVITPOTQSEELKEGNPHLL	2.40
Db	181	RSVSLLPLEFRDSSYELOVRAGPMPGSSYOGTWSBMSDPVITPOTQSEELKEGNPHLL	2.40
Oy	241	LLLLVIVFIPAEWSLKTBPMLRMKIKIAVSPERFPMPLKCGSGFKKMGVAPFTGSS	3.00
Db	241	LLLLVIVFIPAEWSLKTBPMLRMKIKIAVSPERFPMPLKCGSGFKKMGVAPFTGSS	3.00
Oy	301	LEIGPMSPEVPSTLEVYSGHPRPSPAKRLQTLIELQPAELVESGUVKESFWPFAQNQSG	3.60
Db	301	LEIGPMSPEVPSTLEVYSGHPRPSPAKRLQTLIELQPAELVESGUVKESFWPFAQNQSG	3.60
Oy	361	SAYSESRDPPYGVASIDTYTVLDAAGPCTWPCSEBDOCPALDLDADALJBSPGLEPDL	4.20
Db	361	SAYSESRDPPYGVASIDTYTVLDAAGPCTWPCSEBDOCPALDLDADALJBSPGLEPDL	4.20
Oy	421	AGTTVLSGCVSAGSPGLGPGLSLLDLRKPLADGEDMAGCLPWGGRSPGVSESEAGS	4.80
Db	421	AGTTVLSGCVSAGSPGLGPGLSLLDLRKPLADGEDMAGCLPWGGRSPGVSESEAGS	4.80
Oy	481	PLAGLMDPFDGSPGSCSSPVEDCFPSPCDDEBPSPSYLRQWVITPPPLSSGPQAS	5.38
Db	481	PLAGLMDPFDGSPGSCSSPVEDCFPSPCDDEBPSPSYLRQWVITPPPLSSGPQAS	5.38

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1  RESULT 3
2  US-09-404-641-2
3  Sequence 2, Application US/09404641
4  Patent No. 6576744
5  GENERAL INFORMATION:
6  APPLICANT: Presnell, Scott R.
7  APPLICANT: Presnell, Darrell C.
8  APPLICANT: No. 6576744ak, Julia E.
9  APPLICANT: Hammond, Angela K.
10 TITLE OF INVENTION: CYTOKINE RECEPTOR ZAP70A11
11 FILE REFERENCE: 98-55
12 CURRENT APPLICATION NUMBER: US/09/404,641
13 CURRENT FILING DATE: 1999-09-23
14 PRIOR APPLICATION NUMBER: US 60/100,896
15 PRIOR FILING DATE: 1998-09-23
16 PRIOR APPLICATION NUMBER: US 60/123,546
17 PRIOR FILING DATE: 1999-03-09
18 PRIOR APPLICATION NUMBER: US 60/142,574
19 PRIOR FILING DATE: 1999-07-06
20 NUMBER OF SEQ ID NOS: 91
21 SOFTWARE: FastSeq for Windows Version 3.0
22 SEQ ID NO 2
23 LENGTH: 538
24 TYPE: PRT
25 ORGANISM: Homo sapiens
26 US-09-404-641-2

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Query Match	100.0%;	Score 2958;	DB 2;	Length 538;
Best Local Similarity	100.0%;	Pred. No. 3.6e-267;		
Matches 538;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Db
1 MPRGMAAPLLLLLLGCGNCPPDLVCYTDYLQIVICILEMMNLHPSTLTITWQDQYEELKD 60

Oy 61 EATSCSLHRSAHNAHTAATTYCHMDVFEHPMADIPSVNITDQSGNVSECCGFLAAISIKP 120
Db 61 EATSCSLHRSAHNAHTAATTYCHMDVFEHPMADI FSVNITDQSGNVSECCGFLAAISIKP 120

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DB 121 APPENVTVTSSGOYNTISWRSDEYEDPAFYMLKGKLOVELQYRNRGDPMVAVSRRKLISVDS 180
QY 181 RSVSLPLERFKOSSYELQYRAGPMPGSSYQGTWSEMSDVIFQTOSEELKEGNPHLL 240
DB 181 RSVSLPLERFKOSSYELQYRAGPMPGSSYQGTWSEMSDVIFQTOSEELKEGNPHLL 240
QY 241 LLLLVIFIPAFMSLKTPLMLRWKKIWA VSPERFPMPLYKCGSGDFKKVGAFTGSS 300
DB 241 LLLLVIFIPAFMSLKTPLMLRWKKIWA VSPERFPMPLYKCGSGDFKKVGAFTGSS 300
QY 301 LELGPMSPVPSTLEVYSCHPRRSPAKRLDTLQGEPAELVESDGVKPSFWPTAQNSSG 360
DB 301 LELGPMSPVPSTLEVYSCHPRRSPAKRLDTLQGEPAELVESDGVKPSFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCCEDDGYPALDDAGLEBSPGLEDL 420
DB 361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCCEDDGYPALDDAGLEBSPGLEDL 420
QY 421 AGTTVLSGCGVSAGSPGLGPGLSLDRLKRPPLADGEDMAGLPMGGRSPGVSSEBAGS 480
DB 421 AGTTVLSGCGVSAGSPGLGPGLSLDRLKRPPLADGEDMAGLPMGGRSPGVSSEBAGS 480
QY 481 PLAGLMDTDFDSGVSDCSSPVECDFTSPQDEBGPSPSYLRQWVVIIPPLSSPGPQAS 538
DB 481 PLAGLMDTDFDSGVSDCSSPVECDFTSPQDEBGPSPSYLRQWVVIIPPLSSPGPQAS 538
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RESULT 4
US-09-923-246-115
Sequence 115, Application US/09923246
Patent No. 6605272

GENERAL INFORMATION:

```
APPLICANT: No. 6605272a, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923, 246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522, 217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123, 904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142, 013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-09-923-246-115
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Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3,6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGMAAPLLLLLLQGGWGCBDLVCTYDTYICILEMNLHPSLTLLTQDOYEBELKD 60
DB 1 MPRGMAAPLLLLLLQGGWGCBDLVCTYDTYICILEMNLHPSLTLLTQDOYEBELKD 60
QY 61 EATSCSLHRSANHTATYTCMDVPHFMADDFSVNITDQSGNYSOECGSLAESTIKP 120
DB 61 EATSCSLHRSANHTATYTCMDVPHFMADDFSVNITDQSGNYSOECGSLAESTIKP 120
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QY 121 APPENVTVTSSGOYNTISWRSDEYEDPAFYMLKGKLOVELQYRNRGDPMVAVSRRKLISVDS 180
DB 121 APPENVTVTSSGOYNTISWRSDEYEDPAFYMLKGKLOVELQYRNRGDPMVAVSRRKLISVDS 180
QY 181 RSVSLPLERFKOSSYELQYRAGPMPGSSYQGTWSEMSDVIFQTOSEELKEGNPHLL 240
DB 181 RSVSLPLERFKOSSYELQYRAGPMPGSSYQGTWSEMSDVIFQTOSEELKEGNPHLL 240
QY 241 LLLLVIFIPAFMSLKTPLMLRWKKIWA VSPERFPMPLYKCGSGDFKKVGAFTGSS 300
DB 241 LLLLVIFIPAFMSLKTPLMLRWKKIWA VSPERFPMPLYKCGSGDFKKVGAFTGSS 300
QY 301 LELGPMSPVPSTLEVYSCHPRRSPAKRLDTLQGEPAELVESDGVKPSFWPTAQNSSG 360
DB 301 LELGPMSPVPSTLEVYSCHPRRSPAKRLDTLQGEPAELVESDGVKPSFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCCEDDGYPALDDAGLEBSPGLEDL 420
DB 361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCCEDDGYPALDDAGLEBSPGLEDL 420
QY 421 AGTTVLSGCGVSAGSPGLGPGLSLDRLKRPPLADGEDMAGLPMGGRSPGVSSEBAGS 480
DB 421 AGTTVLSGCGVSAGSPGLGPGLSLDRLKRPPLADGEDMAGLPMGGRSPGVSSEBAGS 480
QY 481 PLAGLMDTDFDSGVSDCSSPVECDFTSPQDEBGPSPSYLRQWVVIIPPLSSPGPQAS 538
DB 481 PLAGLMDTDFDSGVSDCSSPVECDFTSPQDEBGPSPSYLRQWVVIIPPLSSPGPQAS 538
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RESULT 5
US-10-295-723-115
Sequence 115, Application US/10295723
Patent No. 6686178

GENERAL INFORMATION:

```
APPLICANT: No. 6686178a, Julia E.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295, 723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522, 217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123, 547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123, 904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142, 013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-723-115
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Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3,6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGMAAPLLLLLLQGGWGCBDLVCTYDTYICILEMNLHPSLTLLTQDOYEBELKD 60
DB 1 MPRGMAAPLLLLLLQGGWGCBDLVCTYDTYICILEMNLHPSLTLLTQDOYEBELKD 60
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QY 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQEGCSFLLAESIKP 120
| | | | |
Db 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQEGCSFLLAESIKP 120
QY 121 APPENVTVTFSGOYNISWRSDEYEDPAFYMLKGKLYELQYRNKGDPMVAVSPPRKLISVDS 180
| | | | |
Db 121 APPENVTVTFSGOYNISWRSDEYEDPAFYMLKGKLYELQYRNKGDPMVAVSPPRKLISVDS 180
QY 181 RSVALPLERKDSSEYELQYRAGMPGSSYQGTWSEMSDVIIFQTSSEELKEGNPHLL 240
| | | | |
Db 181 RSVALPLERKDSSEYELQYRAGMPGSSYQGTWSEMSDVIIFQTSSEELKEGNPHLL 240
QY 241 LLLLVIFIPAFMSLKTHPRLMKKIWAVSPERFMPLYKCGSGDFKKNVGAFFTGSS 300
| | | | |
Db 241 LLLLVIFIPAFMSLKTHPRLMKKIWAVSPERFMPLYKCGSGDFKKNVGAFFTGSS 300
QY 301 LELGPMSEVPSTLEVYSCHPPRSAPAKRLQUTLEQPAELVESDGVKPSFMPAQNOSCG 360
| | | | |
Db 301 LELGPMSEVPSTLEVYSCHPPRSAPAKRLQUTLEQPAELVESDGVKPSFMPAQNOSCG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADGLEBSPGLEPDL 420
| | | | |
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADGLEBSPGLEPDL 420
QY 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGLPMGGRSPGVSESEAGS 480
| | | | |
Db 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPQAS 538
| | | | |
Db 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPQAS 538
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RESULT 6
US-10-414-186-2
; Sequence 2, Application US/10414186
; Patent No. 6692924
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6692924ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPPAH11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-414-186-2
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Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3, 6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGMAAPLULLLLLOGMGCPDLVCYTDYQTYICILEMMNLHPSSTLTLMQOYEEKLD 60
| | | | |
Db 1 MPRGMAAPLULLLLLOGMGCPDLVCYTDYQTYICILEMMNLHPSSTLTLMQOYEEKLD 60
QY 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQEGCSFLLAESIKP 120
| | | | |
Db 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQEGCSFLLAESIKP 120
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QY 121 APPENVTVTFSGOYNISWRSDEYEDPAFYMLKGKLYELQYRNKGDPMVAVSPPRKLISVDS 180
| | | | |
Db 121 APPENVTVTFSGOYNISWRSDEYEDPAFYMLKGKLYELQYRNKGDPMVAVSPPRKLISVDS 180
QY 181 RSVALPLERKDSSEYELQYRAGMPGSSYQGTWSEMSDVIIFQTSSEELKEGNPHLL 240
| | | | |
Db 181 RSVALPLERKDSSEYELQYRAGMPGSSYQGTWSEMSDVIIFQTSSEELKEGNPHLL 240
QY 241 LLLLVIFIPAFMSLKTHPRLMKKIWAVSPERFMPLYKCGSGDFKKNVGAFFTGSS 300
| | | | |
Db 241 LLLLVIFIPAFMSLKTHPRLMKKIWAVSPERFMPLYKCGSGDFKKNVGAFFTGSS 300
QY 301 LELGPMSEVPSTLEVYSCHPPRSAPAKRLQUTLEQPAELVESDGVKPSFMPAQNOSCG 360
| | | | |
Db 301 LELGPMSEVPSTLEVYSCHPPRSAPAKRLQUTLEQPAELVESDGVKPSFMPAQNOSCG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADGLEBSPGLEPDL 420
| | | | |
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADGLEBSPGLEPDL 420
QY 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGLPMGGRSPGVSESEAGS 480
| | | | |
Db 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPQAS 538
| | | | |
Db 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPQAS 538
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RESULT 7
US-09-825-561A-2
; Sequence 2, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZAPPAH11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-2
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Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3, 6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGMAAPLULLLLLOGMGCPDLVCYTDYQTYICILEMMNLHPSSTLTLMQOYEEKLD 60
| | | | |
Db 1 MPRGMAAPLULLLLLOGMGCPDLVCYTDYQTYICILEMMNLHPSSTLTLMQOYEEKLD 60
QY 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQEGCSFLLAESIKP 120
| | | | |
Db 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQEGCSFLLAESIKP 120
QY 121 APPENVTVTFSGOYNISWRSDEYEDPAFYMLKGKLYELQYRNKGDPMVAVSPPRKLISVDS 180
| | | | |
Db 121 APPENVTVTFSGOYNISWRSDEYEDPAFYMLKGKLYELQYRNKGDPMVAVSPPRKLISVDS 180
```

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QY 181 RSVSLLPLEFRKDSYELQVRAGPMPGSSYOGTWSWSDPVI FQTQSEBELKEGNNPHLL 240
DB 181 RSVSLLPLEFRKDSYELQVRAGPMPGSSYOGTWSWSDPVI FQTQSEBELKEGNNPHLL 240
QY 241 LLLIVIVIPAFWMLKTHPLRLMKKIWA VSPERFPMPL YKGCSDGDKKVVGAFTGSS 300
DB 241 LLLIVIVIPAFWMLKTHPLRLMKKIWA VSPERFPMPL YKGCSDGDKKVVGAFTGSS 300
QY 301 LELGPMSEVSTLEVYSCHPPRSPAKRLQ LTELQEPALVESDGVPRKSPWPTAQNCGG 360
DB 301 LELGPMSEVSTLEVYSCHPPRSPAKRLQ LTELQEPALVESDGVPRKSPWPTAQNCGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCEDDGPALDLDAGLEPSPGLEDPLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCEDDGPALDLDAGLEPSPGLEDPLD 420
QY 421 AGTVLSCGCVSAGSPGLGCPGLSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTVLSCGCVSAGSPGLGCPGLSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFVSGDCCSPVECDFTSPGDEGPPRSYLQWVVI PPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFVSGDCCSPVECDFTSPGDEGPPRSYLQWVVI PPPLSSPGPOAS 538
```

```
RESULT 8
US-10-243-072-2
; Sequence 2, Application US/10243072
; Patent No. 6803451
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
; APPLICANT: Conklin, Dorell C.
; APPLICANT: No. 6803451a, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-555C1
; CURRENT APPLICATION NUMBER: US/10/243.072
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-072-2
```

Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3.6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGMAAPL LLLLLQGGMGCPDLVCYTDYLTQTVICILEMNNLHPSTLTTLTWMQDQYEBLKD 60
DB 1 MPRGMAAPL LLLLLQGGMGCPDLVCYTDYLTQTVICILEMNNLHPSTLTTLTWMQDQYEBLKD 60
QY 61 EATCSLHRSANNAHTATYTCMDVFFHMAADIFSVNTTDSGNYSOCGSGFLAESTIKP 120
DB 61 EATCSLHRSANNAHTATYTCMDVFFHMAADIFSVNTTDSGNYSOCGSGFLAESTIKP 120
QY 121 APPFNVTYTFSGQYNI SWRSDEYEDPAFYMLKGKLO YELQYRNKGDPMVA SPRKLI SYDS 180
DB 121 APPFNVTYTFSGQYNI SWRSDEYEDPAFYMLKGKLO YELQYRNKGDPMVA SPRKLI SYDS 180
QY 181 RSVSLLPLEFRKDSYELQVRAGPMPGSSYOGTWSWSDPVI FQTQSEBELKEGNNPHLL 240
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DB 181 RSVSLLPLEFRKDSYELQVRAGPMPGSSYOGTWSWSDPVI FQTQSEBELKEGNNPHLL 240
QY 241 LLLIVIVIPAFWMLKTHPLRLMKKIWA VSPERFPMPL YKGCSDGDKKVVGAFTGSS 300
DB 241 LLLIVIVIPAFWMLKTHPLRLMKKIWA VSPERFPMPL YKGCSDGDKKVVGAFTGSS 300
QY 301 LELGPMSEVSTLEVYSCHPPRSPAKRLQ LTELQEPALVESDGVPRKSPWPTAQNCGG 360
DB 301 LELGPMSEVSTLEVYSCHPPRSPAKRLQ LTELQEPALVESDGVPRKSPWPTAQNCGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCEDDGPALDLDAGLEPSPGLEDPLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCEDDGPALDLDAGLEPSPGLEDPLD 420
QY 421 AGTVLSCGCVSAGSPGLGCPGLSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTVLSCGCVSAGSPGLGCPGLSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFVSGDCCSPVECDFTSPGDEGPPRSYLQWVVI PPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFVSGDCCSPVECDFTSPGDEGPPRSYLQWVVI PPPLSSPGPOAS 538
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RESULT 9
US-10-282-622-16
; Sequence 16, Application US/10282622
; Patent No. 6929932
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. 6929932a, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282.622
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-622-16
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Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3.6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGMAAPL LLLLLQGGMGCPDLVCYTDYLTQTVICILEMNNLHPSTLTTLTWMQDQYEBLKD 60
DB 1 MPRGMAAPL LLLLLQGGMGCPDLVCYTDYLTQTVICILEMNNLHPSTLTTLTWMQDQYEBLKD 60
QY 61 EATCSLHRSANNAHTATYTCMDVFFHMAADIFSVNTTDSGNYSOCGSGFLAESTIKP 120
DB 61 EATCSLHRSANNAHTATYTCMDVFFHMAADIFSVNTTDSGNYSOCGSGFLAESTIKP 120
QY 121 APPFNVTYTFSGQYNI SWRSDEYEDPAFYMLKGKLO YELQYRNKGDPMVA SPRKLI SYDS 180
DB 121 APPFNVTYTFSGQYNI SWRSDEYEDPAFYMLKGKLO YELQYRNKGDPMVA SPRKLI SYDS 180
QY 181 RSVSLLPLEFRKDSYELQVRAGPMPGSSYOGTWSWSDPVI FQTQSEBELKEGNNPHLL 240
DB 181 RSVSLLPLEFRKDSYELQVRAGPMPGSSYOGTWSWSDPVI FQTQSEBELKEGNNPHLL 240
QY 241 LLLIVIVIPAFWMLKTHPLRLMKKIWA VSPERFPMPL YKGCSDGDKKVVGAFTGSS 300
DB 241 LLLIVIVIPAFWMLKTHPLRLMKKIWA VSPERFPMPL YKGCSDGDKKVVGAFTGSS 300
QY 301 LELGPMSEVSTLEVYSCHPPRSPAKRLQ LTELQEPALVESDGVPRKSPWPTAQNCGG 360
DB 301 LELGPMSEVSTLEVYSCHPPRSPAKRLQ LTELQEPALVESDGVPRKSPWPTAQNCGG 360
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Qy 361 SAYSEEDRPVGLVSIIDVTVTLDAGPCTPSCCEDDGYPALDLDAGLESPGLJEDPLD 420
Db 361 SAYSEEDRPVGLVSIIDVTVTLDAGPCTPSCCEDDGYPALDLDAGLESPGLJEDPLD 420
Qy 421 AGTVLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
Db 421 AGTVLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
Qy 481 PLAGLMDTDFSDGSGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPEPLSSPGPOAS 538
Db 481 PLAGLMDTDFSDGSGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPEPLSSPGPOAS 538

RESULT 10
US-09-949-016-11544
; Sequence 11544, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11544
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11544

Query Match 100.0%; Score 2958; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 3.6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGMAAPLLLLLLGSGMGPDLVCYTDYLOTVICILEMNLHPSSTLTLLTMDQYEBKD 60
Db 1 MPRGMAAPLLLLLLGSGMGPDLVCYTDYLOTVICILEMNLHPSSTLTLLTMDQYEBKD 69
Qy 61 EATSCSLHRSANATHATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLLAESIKP 120
Db 70 EATSCSLHRSANATHATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLLAESIKP 129
Qy 121 APPENVTVTSGQYNIWSRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLIYSVS 180
Db 130 APPENVTVTSGQYNIWSRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLIYSVS 189
Qy 181 RVSYSILPLERKDSYELQVAPGMPGSSYQGTWSEMSDPVIFOTOSSELKEGNNPHLL 240
Db 190 RVSYSILPLERKDSYELQVAPGMPGSSYQGTWSEMSDPVIFOTOSSELKEGNNPHLL 249
Qy 241 LLLLVIVIFAPFWSLKTPLRLMKKIWAIVSPERFEMPLYKCGSGDFKKNVGAFTGSS 300
Db 250 LLLLVIVIFAPFWSLKTPLRLMKKIWAIVSPERFEMPLYKCGSGDFKKNVGAFTGSS 309
Qy 301 LEIGPMSPEVYSTLEVSYCHPSPSPAKRLQITELQEPALVESDGVKPSFTWPTAQNCGG 360
Db 310 LEIGPMSPEVYSTLEVSYCHPSPSPAKRLQITELQEPALVESDGVKPSFTWPTAQNCGG 369
Qy 361 SAYSEEDRPVGLVSIIDVTVTLDAGPCTPSCCEDDGYPALDLDAGLESPGLJEDPLD 420
Db 370 SAYSEEDRPVGLVSIIDVTVTLDAGPCTPSCCEDDGYPALDLDAGLESPGLJEDPLD 429
Qy 421 AGTVLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
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Db 430 AGTVLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 489
Qy 481 PLAGLMDTDFSDGSGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPEPLSSPGPOAS 538
Db 490 PLAGLMDTDFSDGSGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPEPLSSPGPOAS 547

RESULT 11
US-09-825-561A-65
; Sequence 65, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 568
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-825-561A-65

Query Match 95.2%; Score 2817; DB 2; Length 568;
Best Local Similarity 89.9%; Pred. No. 5.6e-254;
Matches 523; Conservative 0; Mismatches 1; Indels 58; Gaps 3;

Qy 1 MPRGMAAPLLLLLLGSGMGPDLVCYTDYLOTVICILEMNLHPSSTLTLLTMDQYEBKD 60
Db 1 MPRGMAAPLLLLLLGSGMGPDLVCYTDYLOTVICILEMNLHPSSTLTLLTMDQYEBKD 69
Qy 35 CILEMNLHPSSTLTLLTMDQYEBKD-----QDYELKDEATSCSLHRSANATH 76
Db 61 CILEMNLHPSSTLTLLTMDQYEBKD-----QDYELKDEATSCSLHRSANATH 120
Qy 77 ATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLLAESIKPAPPENVTVTSGQYNI 136
Db 121 ATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLLAESIKPAPPENVTVTSGQYNI 166
Qy 137 SWSRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLIYSVSRSYSLPLEFRKDSY 196
Db 167 SWSRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLIYSVSRSYSLPLEFRKDSY 226
Qy 197 ELQVAPGMPGSSYQGTWSEMSDPVIFOTOSSELKEGNNPHLLLLLVIVIFAPFWSLK 256
Db 227 ELQVAPGMPGSSYQGTWSEMSDPVIFOTOSSELKEGNNPHLLLLLVIVIFAPFWSLK 286
Qy 287 THPLRLMKKIWAIVSPERFEMPLYKCGSGDFKKNVGAFTGSSILEIGPMSPEVYSTLEV 346
Db 257 THPLRLMKKIWAIVSPERFEMPLYKCGSGDFKKNVGAFTGSSILEIGPMSPEVYSTLEV 316
Qy 317 YSCHPSPSPAKRLQITELQEPALVESDGVKPSFTWPTAQNCGSASAYSEEDRPVGLVSI 376
Db 347 YSCHPSPSPAKRLQITELQEPALVESDGVKPSFTWPTAQNCGSASAYSEEDRPVGLVSI 406
Qy 407 DYTIVLDAGPCTPSCCEDDGYPALDLDAGLESPGLJEDPLDAGTVLSCGCVSAGSP 436
Db 437 DYTIVLDAGPCTPSCCEDDGYPALDLDAGLESPGLJEDPLDAGTVLSCGCVSAGSP 466
Qy 467 GLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGSPLAGLMDTDFSDGSGV 526
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Qy 497 SDGSPVECDTTSRQDEGPPRSYLRQWVVIIPPLSSPGPOAS 538
Db 527 SDGSPVECDTTSRQDEGPPRSYLRQWVVIIPPLSSPGPOAS 568

RESULT 12

US-09-404-641-85
; Sequence 85, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6576744ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPPAH11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-404-641-85

Query Match 58.7%; Score 1735.5; DB 2; Length 529;
Best Local Similarity 62.7%; Pred. No. 4.6e-153;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

Qy 1 MPRGMAAPLILLILQGGMGCPDLVCYTDYLOTVCILEMNLHPSTLTLMQDOYEELKD 60
Db 1 MPRGPAVALILLILHGAWSCLDLTCTYTDYLTITCTVLETRSPNPISLTLMQDEYEELQD 60
Qy 61 EATCSLHRSANMTHATYTCMDVHFHMADDFSVNTDOSGNVSOCSGFFLAESIKP 120
Db 61 QETCSLHRSANMTHATYTCMDVHFHMADDFSVNTDOSGNVSOCSGFFLAESIKP 120
Qy 121 APPENVVTFSGOVYISWRSDYEDPAFMYLKGKLOYLEQYRNRGDPMVAVSPRKLISVDS 180
Db 121 APPENVVTFSGOVYISWRSDYEDPAFMYLKGKLOYLEQYRNRGDPMVAVSPRKLISVDS 180
Qy 121 APPENVVTFSGOVYISWRSDYEDPAFMYLKGKLOYLEQYRNRGDPMVAVSPRKLISVDS 180
Db 121 APPENVVTFSGOVYISWRSDYEDPAFMYLKGKLOYLEQYRNRGDPMVAVSPRKLISVDS 180
Qy 181 RSVSLPLEFRKDSYELQVRAQPMGSSYOGTSEMSDPVI FQTQSEELKEGNNPHLL 240
Db 181 RSVSLPLEFRKDSYELQVRAQPMGSSYOGTSEMSDPVI FQTQSEELKEGNNPHLL 240
Qy 241 LLLLVYVTFPMSLKTHTPLRLMKKIWA-VPSERRFPMPLKYGSGGPFKKVGAAPFTGS 299
Db 241 LLLLVYVTFPMSLKTHTPLRLMKKIWA-VPSERRFPMPLKYGSGGPFKKVGAAPFTGS 299
Qy 241 LLLLVYVTFPMSLKTHTPLRLMKKIWA-VPSERRFPMPLKYGSGGPFKKVGAAPFTGS 299
Db 241 LLLLVYVTFPMSLKTHTPLRLMKKIWA-VPSERRFPMPLKYGSGGPFKKVGAAPFTGS 299
Qy 300 SLEIGPMSEVSTLEVYSCHPSPAPAKRLQTLTQEBPAELVESDGVKPSFW--PTAQ 356
Db 300 SLEIGPMSEVSTLEVYSCHPSPAPAKRLQTLTQEBPAELVESDGVKPSFW--PTAQ 356
Qy 300 SLEIGPMSEVSTLEVYSCHPSPAPAKRLQTLTQEBPAELVESDGVKPSFW--PTAQ 356
Db 300 SLEIGPMSEVSTLEVYSCHPSPAPAKRLQTLTQEBPAELVESDGVKPSFW--PTAQ 356
Qy 357 NSGSAVSEERDRPYGLVSDITVTVLDAEGPCTMPCSCEDDGYPALDLDALESPGLEAD 416
Db 357 NSGSAVSEERDRPYGLVSDITVTVLDAEGPCTMPCSCEDDGYPALDLDALESPGLEAD 416
Qy 355 GQAVSAVSEERDRPYGLVSDITVTVLDAEGPCTMPCSCEDDGYPALDLDALESPGLEAD 414
Db 355 GQAVSAVSEERDRPYGLVSDITVTVLDAEGPCTMPCSCEDDGYPALDLDALESPGLEAD 414
Qy 417 PLUDAGTIVLSCGCVSAGSPGLGSLDLRLKPLADGEMWAGLPMWGRSGGVSES 476
Db 417 PLUDAGTIVLSCGCVSAGSPGLGSLDLRLKPLADGEMWAGLPMWGRSGGVSES 476
Qy 415 LLLVTPAFLSCGCVSAGSPGLGSLDLRLKPLADGEMWAGLPMWGRSGGVSES 474
Db 415 LLLVTPAFLSCGCVSAGSPGLGSLDLRLKPLADGEMWAGLPMWGRSGGVSES 474
Qy 477 EAGSPPLAGLMDTDFSGFVSGSDSPVECDTTSRQDEGPPRSYLRQWVVIIPPLSSPGPO 536
Db 477 EAGSPPLAGLMDTDFSGFVSGSDSPVECDTTSRQDEGPPRSYLRQWVVIIPPLSSPGPO 536
Qy 475 EAGSP-PLDMDTDFSGFVSGSDSPVECDTTSRQDEGPPRSYLRQWVVIIPPLSSPGPO 527
Db 475 EAGSP-PLDMDTDFSGFVSGSDSPVECDTTSRQDEGPPRSYLRQWVVIIPPLSSPGPO 527

Qy 537 AS 538
Db 528 SS 529

RESULT 13

US-10-414-186-85
; Sequence 85, Application US/10414186
; Patent No. 6692924
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6692924ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPPAH11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-414-186-85

Query Match 58.7%; Score 1735.5; DB 2; Length 529;
Best Local Similarity 62.7%; Pred. No. 4.6e-153;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

Qy 1 MPRGMAAPLILLILQGGMGCPDLVCYTDYLOTVCILEMNLHPSTLTLMQDOYEELKD 60
Db 1 MPRGPAVALILLILHGAWSCLDLTCTYTDYLTITCTVLETRSPNPISLTLMQDEYEELQD 60
Qy 61 EATCSLHRSANMTHATYTCMDVHFHMADDFSVNTDOSGNVSOCSGFFLAESIKP 120
Db 61 QETCSLHRSANMTHATYTCMDVHFHMADDFSVNTDOSGNVSOCSGFFLAESIKP 120
Qy 121 APPENVVTFSGOVYISWRSDYEDPAFMYLKGKLOYLEQYRNRGDPMVAVSPRKLISVDS 180
Db 121 APPENVVTFSGOVYISWRSDYEDPAFMYLKGKLOYLEQYRNRGDPMVAVSPRKLISVDS 180
Qy 121 APPENVVTFSGOVYISWRSDYEDPAFMYLKGKLOYLEQYRNRGDPMVAVSPRKLISVDS 180
Db 121 APPENVVTFSGOVYISWRSDYEDPAFMYLKGKLOYLEQYRNRGDPMVAVSPRKLISVDS 180
Qy 181 RSVSLPLEFRKDSYELQVRAQPMGSSYOGTSEMSDPVI FQTQSEELKEGNNPHLL 240
Db 181 RSVSLPLEFRKDSYELQVRAQPMGSSYOGTSEMSDPVI FQTQSEELKEGNNPHLL 240
Qy 241 LLLLVYVTFPMSLKTHTPLRLMKKIWA-VPSERRFPMPLKYGSGGPFKKVGAAPFTGS 299
Db 241 LLLLVYVTFPMSLKTHTPLRLMKKIWA-VPSERRFPMPLKYGSGGPFKKVGAAPFTGS 299
Qy 241 LLLLVYVTFPMSLKTHTPLRLMKKIWA-VPSERRFPMPLKYGSGGPFKKVGAAPFTGS 299
Db 241 LLLLVYVTFPMSLKTHTPLRLMKKIWA-VPSERRFPMPLKYGSGGPFKKVGAAPFTGS 299
Qy 300 SLEIGPMSEVSTLEVYSCHPSPAPAKRLQTLTQEBPAELVESDGVKPSFW--PTAQ 356
Db 300 SLEIGPMSEVSTLEVYSCHPSPAPAKRLQTLTQEBPAELVESDGVKPSFW--PTAQ 356
Qy 300 SLEIGPMSEVSTLEVYSCHPSPAPAKRLQTLTQEBPAELVESDGVKPSFW--PTAQ 356
Db 300 SLEIGPMSEVSTLEVYSCHPSPAPAKRLQTLTQEBPAELVESDGVKPSFW--PTAQ 356
Qy 357 NSGSAVSEERDRPYGLVSDITVTVLDAEGPCTMPCSCEDDGYPALDLDALESPGLEAD 416
Db 357 NSGSAVSEERDRPYGLVSDITVTVLDAEGPCTMPCSCEDDGYPALDLDALESPGLEAD 416
Qy 355 GQAVSAVSEERDRPYGLVSDITVTVLDAEGPCTMPCSCEDDGYPALDLDALESPGLEAD 414
Db 355 GQAVSAVSEERDRPYGLVSDITVTVLDAEGPCTMPCSCEDDGYPALDLDALESPGLEAD 414
Qy 417 PLUDAGTIVLSCGCVSAGSPGLGSLDLRLKPLADGEMWAGLPMWGRSGGVSES 476
Db 417 PLUDAGTIVLSCGCVSAGSPGLGSLDLRLKPLADGEMWAGLPMWGRSGGVSES 476
Qy 415 LLLVTPAFLSCGCVSAGSPGLGSLDLRLKPLADGEMWAGLPMWGRSGGVSES 474
Db 415 LLLVTPAFLSCGCVSAGSPGLGSLDLRLKPLADGEMWAGLPMWGRSGGVSES 474
Qy 477 EAGSPPLAGLMDTDFSGFVSGSDSPVECDTTSRQDEGPPRSYLRQWVVIIPPLSSPGPO 536
Db 477 EAGSPPLAGLMDTDFSGFVSGSDSPVECDTTSRQDEGPPRSYLRQWVVIIPPLSSPGPO 536
Qy 475 EAGSP-PLDMDTDFSGFVSGSDSPVECDTTSRQDEGPPRSYLRQWVVIIPPLSSPGPO 527
Db 475 EAGSP-PLDMDTDFSGFVSGSDSPVECDTTSRQDEGPPRSYLRQWVVIIPPLSSPGPO 527

Oy 537 AS 538
: |
Db 528 SS 529

RESULT 14
US-09-825-561A-12
; Sequence 12, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: Meast, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 529
; TYPE: PRT
; ORGANISM: mus musculus
US-09-825-561A-12

Query Match 58.7%; Score 1735.5; DB 2; Length 529;
Best Local Similarity 62.7%; Pred. No. 4.6e-153;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

Oy 1 MPRGMAPLLILLLOGGMGCPDLYCYDYIQTIVICILEMNNLHSTLTTLTMOQYBELKD 60
1 MPRGPVALLLILLHGMASCLDLTCYDYLTITVLETSPNSISLTLMODEYBELKD 60
Db 1 MPRGPVALLLILLHGMASCLDLTCYDYLTITVLETSPNSISLTLMODEYBELKD 60
Oy 61 EATSCSLHRSANHTATYTCTHMDVHFHMADIFSVNITDQSGNYSQEGCSFLAESIKP 120
61 QETFCSLHRSNGHNTHTWYCHMRLSGLDEIVANVTQSGNNSQEGCSFVLAESIKP 120
Db 61 EATSCSLHRSNGHNTHTWYCHMRLSGLDEIVANVTQSGNNSQEGCSFVLAESIKP 120
Oy 121 APPPNVTFTSGQYNISMRSDYEDPAFYMKGKLYELQYRNKGDPMVAVSFRRLKLSVDS 180
121 APPPNVTFTSGQYNISMRSDYEDPAFYMKGKLYELQYRNKGDPMVAVSFRRLKLSVDS 180
Db 121 APPPNVTFTSGQYNISMRSDYEDPAFYMKGKLYELQYRNKGDPMVAVSFRRLKLSVDS 180
Oy 181 RSVSLPLEFRKDSYELQVRAGPMGSSYQGTWSEMSDPVIFOTQGEPEAGDPMHLL 240
181 RSVSLPLEFRKDSYELQVRAGPMGSSYQGTWSEMSDPVIFOTQGEPEAGDPMHLL 240
Db 181 RSVSLPLEFRKDSYELQVRAGPMGSSYQGTWSEMSDPVIFOTQGEPEAGDPMHLL 240
Oy 241 LLLLVIFIPAFMSLKTHPLRLMKKIWA-VSPERFEMPLYKGCSDGFKKMGVAPRTGS 299
241 LLLLVIFIPAFMSLKTHPLRLMKKIWA-VSPERFEMPLYKGCSDGFKKMGVAPRTGS 299
Db 241 LLLLVIFIPAFMSLKTHPLRLMKKIWA-VSPERFEMPLYKGCSDGFKKMGVAPRTGS 299
Oy 300 SLEIGPMSPEVSTLELYSCHPPRSPAKRLQTLQEAELVESDGVKPSFW--PTAQ 356
300 SLEIGPMSPEVSTLELYSCHPPRSPAKRLQTLQEAELVESDGVKPSFW--PTAQ 356
Db 300 SLEIGPMSPEVSTLELYSCHPPRSPAKRLQTLQEAELVESDGVKPSFW--PTAQ 356
Oy 357 NSGGSAYSEERDRYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBSPGLE 416
357 NSGGSAYSEERDRYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBSPGLE 416
Db 357 NSGGSAYSEERDRYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBSPGLE 416
Oy 417 PLUDAGTTVSLCCGVASGPGGLGSLDLRLKPLADGEDMAGGLPMWGRSPGVSES 476
417 PLUDAGTTVSLCCGVASGPGGLGSLDLRLKPLADGEDMAGGLPMWGRSPGVSES 476
Db 417 PLUDAGTTVSLCCGVASGPGGLGSLDLRLKPLADGEDMAGGLPMWGRSPGVSES 476
Oy 477 EAGSPPLAGLMDTFTDSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPPLSPGPQ 536
477 EAGSPPLAGLMDTFTDSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPPLSPGPQ 536
Db 477 EAGSPPLAGLMDTFTDSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPPLSPGPQ 536

Oy 537 AS 538
: |
Db 528 SS 529

RESULT 15
US-10-243-072-85
; Sequence 85, Application US/10243072
; Patent No. 6803451
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6803451ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-243-072-85

Query Match 58.7%; Score 1735.5; DB 2; Length 529;
Best Local Similarity 62.7%; Pred. No. 4.6e-153;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

Oy 1 MPRGMAPLLILLLOGGMGCPDLYCYDYIQTIVICILEMNNLHSTLTTLTMOQYBELKD 60
1 MPRGPVALLLILLHGMASCLDLTCYDYLTITVLETSPNSISLTLMODEYBELKD 60
Db 1 MPRGPVALLLILLHGMASCLDLTCYDYLTITVLETSPNSISLTLMODEYBELKD 60
Oy 61 EATSCSLHRSANHTATYTCTHMDVHFHMADIFSVNITDQSGNYSQEGCSFLAESIKP 120
61 QETFCSLHRSNGHNTHTWYCHMRLSGLDEIVANVTQSGNNSQEGCSFVLAESIKP 120
Db 61 EATSCSLHRSANHTATYTCTHMDVHFHMADIFSVNITDQSGNYSQEGCSFLAESIKP 120
Oy 121 APPPNVTFTSGQYNISMRSDYEDPAFYMKGKLYELQYRNKGDPMVAVSFRRLKLSVDS 180
121 APPPNVTFTSGQYNISMRSDYEDPAFYMKGKLYELQYRNKGDPMVAVSFRRLKLSVDS 180
Db 121 APPPNVTFTSGQYNISMRSDYEDPAFYMKGKLYELQYRNKGDPMVAVSFRRLKLSVDS 180
Oy 181 RSVSLPLEFRKDSYELQVRAGPMGSSYQGTWSEMSDPVIFOTQGEPEAGDPMHLL 240
181 RSVSLPLEFRKDSYELQVRAGPMGSSYQGTWSEMSDPVIFOTQGEPEAGDPMHLL 240
Db 181 RSVSLPLEFRKDSYELQVRAGPMGSSYQGTWSEMSDPVIFOTQGEPEAGDPMHLL 240
Oy 241 LLLLVIFIPAFMSLKTHPLRLMKKIWA-VSPERFEMPLYKGCSDGFKKMGVAPRTGS 299
241 LLLLVIFIPAFMSLKTHPLRLMKKIWA-VSPERFEMPLYKGCSDGFKKMGVAPRTGS 299
Db 241 LLLLVIFIPAFMSLKTHPLRLMKKIWA-VSPERFEMPLYKGCSDGFKKMGVAPRTGS 299
Oy 300 SLEIGPMSPEVSTLELYSCHPPRSPAKRLQTLQEAELVESDGVKPSFW--PTAQ 356
300 SLEIGPMSPEVSTLELYSCHPPRSPAKRLQTLQEAELVESDGVKPSFW--PTAQ 356
Db 300 SLEIGPMSPEVSTLELYSCHPPRSPAKRLQTLQEAELVESDGVKPSFW--PTAQ 356
Oy 357 NSGGSAYSEERDRYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBSPGLE 416
357 NSGGSAYSEERDRYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBSPGLE 416
Db 357 NSGGSAYSEERDRYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBSPGLE 416
Oy 417 PLUDAGTTVSLCCGVASGPGGLGSLDLRLKPLADGEDMAGGLPMWGRSPGVSES 476
417 PLUDAGTTVSLCCGVASGPGGLGSLDLRLKPLADGEDMAGGLPMWGRSPGVSES 476
Db 417 PLUDAGTTVSLCCGVASGPGGLGSLDLRLKPLADGEDMAGGLPMWGRSPGVSES 476
Oy 477 EAGSPPLAGLMDTFTDSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPPLSPGPQ 536
477 EAGSPPLAGLMDTFTDSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPPLSPGPQ 536
Db 477 EAGSPPLAGLMDTFTDSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPPLSPGPQ 536

Db	475	EAGSP-PGLDMDITDSGFAGSDCCSPVET-----DSCPPRSYLURONVVRTTPPVDSGAQ	527
Qy	537	AS 538	
	:		
Db	528	SS 529	

Search completed: September 7, 2006, 12:53:37
Job time : 55.8 secs

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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:52:41 ; Search time 195.217 Seconds
(without alignment)
1276.576 Million cell updates/sec

Title: US-10-659-684-115

Perfect score: 2958
Sequence: 1 MPRGMAPLTLILQSGMGC.....YLRQWVYIPPLSPGQAS 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Ceiera_SIDS3/ptodata/2/pubppa/US07_PUBCOMB.pep:*
- 2: /EMC_Ceiera_SIDS3/ptodata/2/pubppa/US06_PUBCOMB.pep:*
- 3: /EMC_Ceiera_SIDS3/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 4: /EMC_Ceiera_SIDS3/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 5: /EMC_Ceiera_SIDS3/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 6: /EMC_Ceiera_SIDS3/ptodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2958	100.0	538	3	US-09-965-313-2
2	2958	100.0	538	3	US-09-923-246-115
3	2958	100.0	538	3	US-09-825-561A-2
4	2958	100.0	538	3	US-09-972-218A-2
5	2958	100.0	538	4	US-10-264-634-2
6	2958	100.0	538	4	US-10-295-723-115
7	2958	100.0	538	4	US-10-282-622-16
8	2958	100.0	538	4	US-10-243-072-2
9	2958	100.0	538	4	US-10-414-186-2
10	2958	100.0	538	4	US-10-456-780-6
11	2958	100.0	538	4	US-10-659-684-115
12	2958	100.0	538	4	US-10-620-169-4
13	2958	100.0	538	4	US-10-715-998-2
14	2958	100.0	538	5	US-10-872-087-2
15	2958	100.0	538	5	US-10-787-442-115
16	2958	100.0	538	5	US-10-798-380-43
17	2958	100.0	538	5	US-10-864-249-2
18	2958	100.0	538	5	US-10-951-239-10
19	2958	100.0	538	6	US-11-174-398-16
20	2958	100.0	538	6	US-11-133-947-6
21	2958	100.0	538	6	US-11-197-488-2
22	2951	99.8	538	3	US-09-758-664-2
23	2817	95.2	568	3	US-09-825-561A-65
24	2817	95.2	568	5	US-10-872-087-65
25	2817	95.2	568	5	US-09-825-561A-12
26	1735.5	58.7	529	3	US-09-972-218A-10
27	1735.5	58.7	529	3	US-09-972-218A-10

28	1735.5	58.7	529	4	US-10-264-634-10	Sequence 10, Appl
29	1735.5	58.7	529	4	US-10-243-072-85	Sequence 85, Appl
30	1735.5	58.7	529	4	US-10-414-186-85	Sequence 85, Appl
31	1735.5	58.7	529	4	US-10-418-450-2	Sequence 2, Appl
32	1735.5	58.7	529	4	US-10-715-998-85	Sequence 85, Appl
33	1735.5	58.7	529	5	US-10-872-087-12	Sequence 12, Appl
34	1735.5	58.7	529	5	US-10-798-380-45	Sequence 45, Appl
35	1735.5	58.7	529	5	US-10-864-249-85	Sequence 85, Appl
36	1735.5	58.7	529	6	US-11-132-947-8	Sequence 8, Appl
37	1735.5	58.7	529	6	US-11-197-488-10	Sequence 10, Appl
38	1729.5	58.5	529	3	US-09-965-313-4	Sequence 4, Appl
39	1729.5	58.5	529	3	US-09-732-234-6	Sequence 6, Appl
40	1729.5	58.5	529	3	US-09-784-859-6	Sequence 6, Appl
41	1729.5	58.5	529	4	US-10-076-840-6	Sequence 6, Appl
42	1729.5	58.5	529	4	US-10-624-044-6	Sequence 6, Appl
43	1729.5	58.5	529	5	US-10-415-440-6	Sequence 6, Appl
44	1591	53.8	289	3	US-09-941-973-2	Sequence 2, Appl
45	1302	44.0	384	6	US-11-075-351-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1									
US-09-965-313-2									
Sequence 2, Application US/09965313									
Patent No. US20020090680A1									
GENERAL INFORMATION:									
APPLICANT: Hodge, Martin R.									
TITLE OF INVENTION: No. US20020090680A1 IL-9/IL-2 Receptor-like Molecules									
FILE REFERENCE: 5800-17A									
CURRENT APPLICATION NUMBER: US/09/965,313									
CURRENT FILING DATE: 2001-09-26									
PRIOR APPLICATION NUMBER: US 09/313,913									
PRIOR FILING DATE: 1999-05-18									
NUMBER OF SEQ ID NOS: 8									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO 2									
LENGTH: 538									
TYPE: PRT									
ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like									
US-09-965-313-2									
Query Match									
Best Local Similarity 100.0%; Score 2958; DB 3; Length 538;									
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MPRGMAPLTLILQSGMGC	PDLYCYDTYVLCILEMNLHPS	TLTLTWODYEELKD	60				
DB	1	MPRGMAPLTLILQSGMGC	PDLYCYDTYVLCILEMNLHPS	TLTLTWODYEELKD	60				
QY	61	EATCSLHRSANHTATYTC	HMDFHFMADDFSVNIT	DQSGNVSOECG	FLLAESIKP	120			
DB	61	EATCSLHRSANHTATYTC	HMDFHFMADDFSVNIT	DQSGNVSOECG	FLLAESIKP	120			
QY	61	EATCSLHRSANHTATYTC	HMDFHFMADDFSVNIT	DQSGNVSOECG	FLLAESIKP	120			
DB	61	EATCSLHRSANHTATYTC	HMDFHFMADDFSVNIT	DQSGNVSOECG	FLLAESIKP	120			
QY	121	APPNNVTYFSGQYINIS	WRSDYEDPAFYMLK	GKLYELQYRN	RDPMAVSPRRKLI	180			
DB	121	APPNNVTYFSGQYINIS	WRSDYEDPAFYMLK	GKLYELQYRN	RDPMAVSPRRKLI	180			
QY	121	APPNNVTYFSGQYINIS	WRSDYEDPAFYMLK	GKLYELQYRN	RDPMAVSPRRKLI	180			
DB	121	APPNNVTYFSGQYINIS	WRSDYEDPAFYMLK	GKLYELQYRN	RDPMAVSPRRKLI	180			
QY	181	RSVGLLPLEPRKDSYEL	QVADGMPGSSVYCG	TSEMSDPVIF	PTQOSELEKGNPHLL	240			
DB	181	RSVGLLPLEPRKDSYEL	QVADGMPGSSVYCG	TSEMSDPVIF	PTQOSELEKGNPHLL	240			
QY	241	LLLVIVIFIPAFWLSL	KTHPLMKKIWA	VPSPFRFMP	LYKSGGDFKKNVGA	300			
DB	241	LLLVIVIFIPAFWLSL	KTHPLMKKIWA	VPSPFRFMP	LYKSGGDFKKNVGA	300			
QY	301	LELQPMSPDVSTLEV	SVCHPSPAPAKLQ	LTLEQEPALVES	GVKPRSPWPTA	360			
DB	301	LELQPMSPDVSTLEV	SVCHPSPAPAKLQ	LTLEQEPALVES	GVKPRSPWPTA	360			
QY	361	SAYSEENRPPYGLV	SIDVTYVTLDAEG	PCTWCSCEDDQY	PALDDAGLEP	420			
DB	361	SAYSEENRPPYGLV	SIDVTYVTLDAEG	PCTWCSCEDDQY	PALDDAGLEP	420			

Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADAGLEBPGLJEDLLD 420
Qy 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMWGRSPGVSESEAGS 480
Db 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMWGRSPGVSESEAGS 480
Qy 481 PLAGLMDTDFDSGVRGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPEPLSSPGPQAS 538
Db 481 PLAGLMDTDFDSGVRGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPEPLSSPGPQAS 538

RESULT 2
US-09-923-246-115
Sequence 115, Application US/09923246
Patent No. US20020128446A1
GENERAL INFORMATION:
APPLICANT: No. US20020128446A1ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Grose, Jane A.
APPLICANT: Johnson, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-09-923-246-115

Query Match 100.0%; Score 2958; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGMAPRLLLLLLOGWMGCPDLVCTDYLOTVICILEMNLHPSTLLTWQDQYEEIKD 60
Db 1 MPRGMAPRLLLLLLOGWMGCPDLVCTDYLOTVICILEMNLHPSTLLTWQDQYEEIKD 60
Qy 61 EATSCSLHRSANAHATYTCMDVHFPMADDFSVNITDQSGNVSOEGCSFLAIESIKP 120
Db 61 EATSCSLHRSANAHATYTCMDVHFPMADDFSVNITDQSGNVSOEGCSFLAIESIKP 120
Qy 121 APPENVTVTFSGQYNISWRSYEDPAFYMLKGKLYELQYLRNCGDPMAVSPRRKLISVDS 180
Db 121 APPENVTVTFSGQYNISWRSYEDPAFYMLKGKLYELQYLRNCGDPMAVSPRRKLISVDS 180
Qy 181 RSVSLPLERFKDSSYELQVRAGMPGSSYQGTWSESDVITQTOSEELKEGNPHLL 240
Db 181 RSVSLPLERFKDSSYELQVRAGMPGSSYQGTWSESDVITQTOSEELKEGNPHLL 240
Qy 241 LLLLVIFIPAFMSLKTPLRLMKKIWAVSPERFEMPLYKGCSDGFKKVVGAAPFTGSS 300
Db 241 LLLLVIFIPAFMSLKTPLRLMKKIWAVSPERFEMPLYKGCSDGFKKVVGAAPFTGSS 300
Qy 301 LEIGPMSPEVPSTLEVYSCHPSPSPAKRLQTELQEPALVESDGVKPSFWPTAQNSSG 360
Db 301 LEIGPMSPEVPSTLEVYSCHPSPSPAKRLQTELQEPALVESDGVKPSFWPTAQNSSG 360

Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADAGLEBPGLJEDLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADAGLEBPGLJEDLLD 420
Qy 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMWGRSPGVSESEAGS 480
Db 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMWGRSPGVSESEAGS 480
Qy 481 PLAGLMDTDFDSGVRGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPEPLSSPGPQAS 538
Db 481 PLAGLMDTDFDSGVRGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPEPLSSPGPQAS 538

RESULT 3
US-09-825-561A-2
Sequence 2, Application US/09825561A
Patent No. US20020137677A1
GENERAL INFORMATION:
APPLICANT: No. US20020137677A1ak, Julia E.
APPLICANT: Sprecher, Cindy A.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-561A-2

Query Match 100.0%; Score 2958; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGMAPRLLLLLLOGWMGCPDLVCTDYLOTVICILEMNLHPSTLLTWQDQYEEIKD 60
Db 1 MPRGMAPRLLLLLLOGWMGCPDLVCTDYLOTVICILEMNLHPSTLLTWQDQYEEIKD 60
Qy 61 EATSCSLHRSANAHATYTCMDVHFPMADDFSVNITDQSGNVSOEGCSFLAIESIKP 120
Db 61 EATSCSLHRSANAHATYTCMDVHFPMADDFSVNITDQSGNVSOEGCSFLAIESIKP 120
Qy 121 APPENVTVTFSGQYNISWRSYEDPAFYMLKGKLYELQYLRNCGDPMAVSPRRKLISVDS 180
Db 121 APPENVTVTFSGQYNISWRSYEDPAFYMLKGKLYELQYLRNCGDPMAVSPRRKLISVDS 180
Qy 181 RSVSLPLERFKDSSYELQVRAGMPGSSYQGTWSESDVITQTOSEELKEGNPHLL 240
Db 181 RSVSLPLERFKDSSYELQVRAGMPGSSYQGTWSESDVITQTOSEELKEGNPHLL 240
Qy 241 LLLLVIFIPAFMSLKTPLRLMKKIWAVSPERFEMPLYKGCSDGFKKVVGAAPFTGSS 300
Db 241 LLLLVIFIPAFMSLKTPLRLMKKIWAVSPERFEMPLYKGCSDGFKKVVGAAPFTGSS 300
Qy 301 LEIGPMSPEVPSTLEVYSCHPSPSPAKRLQTELQEPALVESDGVKPSFWPTAQNSSG 360
Db 301 LEIGPMSPEVPSTLEVYSCHPSPSPAKRLQTELQEPALVESDGVKPSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADAGLEBPGLJEDLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADAGLEBPGLJEDLLD 420
Qy 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMWGRSPGVSESEAGS 480

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Db      421 |||||
Qy      481 PLAGLMDTFDPSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPPGQAS 538
Db      481 PLAGLMDTFDPSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPPGQAS 538

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RESULT 4
US-09-972-218A-2
; Sequence 2, Application US/09972218A
; Publication No. US20030049798A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Laura
; APPLICANT: Whitters, Matthew J
; APPLICANT: Collins, Mary
; APPLICANT: Young, Deborah A.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lowe, Leslie D.
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family
; FILE REFERENCE: 22058-552CIP2
; CURRENT APPLICATION NUMBER: US/09/972,218A
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/569384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/560766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US/6057128
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
US-09-972-218A-2

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Query Match      100.0%; Score 2958; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MPRGMAAPLLLLLQGGMGCPDLVCYTDYQTVICILEMNLHSTLTLTWQDQYEBEKD 60
Qy      61 EATSCSLHRSANHAHTATYTCMDVHFHMDLIFSUNITQSGVSOECSFLAESTIKP 120
Db      61 EATSCSLHRSANHAHTATYTCMDVHFHMDLIFSUNITQSGVSOECSFLAESTIKP 120
Qy      121 APPFNVTFTSGQYINISMRSDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRRLISVDS 180
Db      121 APPFNVTFTSGQYINISMRSDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRRLISVDS 180
Qy      181 RSVALPLERFKOSSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
Db      181 RSVALPLERFKOSSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
Qy      241 LLLLVYFIAPFMSLKTHTPLMRKKTIAVSPERFPMPLKYGSGDFKKWVGAPFTGSS 300
Db      241 LLLLVYFIAPFMSLKTHTPLMRKKTIAVSPERFPMPLKYGSGDFKKWVGAPFTGSS 300
Qy      301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVKPSFMPPTAQNCGG 360
Db      301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVKPSFMPPTAQNCGG 360
Qy      361 SAYSEERDRPYGLVSIITVTYVLDAGPCTWPCSCEDDGYPALDDAGLEBSPGLJEDPLD 420
Db      361 SAYSEERDRPYGLVSIITVTYVLDAGPCTWPCSCEDDGYPALDDAGLEBSPGLJEDPLD 420
Qy      421 AGTTVLSGCGVCSAGSPGLGPGSLDLRLKPLADGEMAGGLPMGGRSPGVSESEAGS 480
Db      421 AGTTVLSGCGVCSAGSPGLGPGSLDLRLKPLADGEMAGGLPMGGRSPGVSESEAGS 480

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Qy      481 PLAGLMDTFDPSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPPGQAS 538
Db      481 PLAGLMDTFDPSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPPGQAS 538

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RESULT 5
US-10-264-634-2
; Sequence 2, Application US/10264634
; Publication No. US20030108549A1
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra et al.
; TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor Activity
; FILE REFERENCE: G15320-P3
; CURRENT APPLICATION NUMBER: US/10/264,634
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 09/040,005
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 09/560,766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/569,384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/972,218
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/373,746
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
US-10-264-634-2

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Query Match      100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MPRGMAAPLLLLLQGGMGCPDLVCYTDYQTVICILEMNLHSTLTLTWQDQYEBEKD 60
Db      1 MPRGMAAPLLLLLQGGMGCPDLVCYTDYQTVICILEMNLHSTLTLTWQDQYEBEKD 60
Qy      61 EATSCSLHRSANHAHTATYTCMDVHFHMDLIFSUNITQSGVSOECSFLAESTIKP 120
Db      61 EATSCSLHRSANHAHTATYTCMDVHFHMDLIFSUNITQSGVSOECSFLAESTIKP 120
Qy      121 APPFNVTFTSGQYINISMRSDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRRLISVDS 180
Db      121 APPFNVTFTSGQYINISMRSDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRRLISVDS 180
Qy      181 RSVALPLERFKOSSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
Db      181 RSVALPLERFKOSSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
Qy      241 LLLLVYFIAPFMSLKTHTPLMRKKTIAVSPERFPMPLKYGSGDFKKWVGAPFTGSS 300
Db      241 LLLLVYFIAPFMSLKTHTPLMRKKTIAVSPERFPMPLKYGSGDFKKWVGAPFTGSS 300
Qy      301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVKPSFMPPTAQNCGG 360
Db      301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVKPSFMPPTAQNCGG 360
Qy      361 SAYSEERDRPYGLVSIITVTYVLDAGPCTWPCSCEDDGYPALDDAGLEBSPGLJEDPLD 420
Db      361 SAYSEERDRPYGLVSIITVTYVLDAGPCTWPCSCEDDGYPALDDAGLEBSPGLJEDPLD 420
Qy      421 AGTTVLSGCGVCSAGSPGLGPGSLDLRLKPLADGEMAGGLPMGGRSPGVSESEAGS 480
Db      421 AGTTVLSGCGVCSAGSPGLGPGSLDLRLKPLADGEMAGGLPMGGRSPGVSESEAGS 480
Qy      481 PLAGLMDTFDPSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPPGQAS 538
Db      481 PLAGLMDTFDPSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPPGQAS 538

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RESULT 6
US-10-295-723-115
; Sequence 115, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-115
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Query Match 100.0%; Score 2958; DB 4; Length 538;

Best Local Similarity 100.0%; Pred. No. 2,8e-228; Mismatches 0; Indels 0; Gaps 0;

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Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGMAAPLLLLLLLOGGMGCPDVCYTDYLOTVICILEMNNLHPSTLTLMQDOYBELKD 60
DB 1 MPRGMAAPLLLLLLLOGGMGCPDVCYTDYLOTVICILEMNNLHPSTLTLMQDOYBELKD 60
QY 61 EATSCSLHRSAHNATHATYTCMDVHFHMADIFSVNITDQSGVYSGECSFLAIESIKP 120
DB 61 EATSCSLHRSAHNATHATYTCMDVHFHMADIFSVNITDQSGVYSGECSFLAIESIKP 120
QY 121 APPNNVTFTSGQYNISWRSYEDPAFYMLKGKLYELQYRNKRDPMVAVSRRKLISVDS 180
DB 121 APPNNVTFTSGQYNISWRSYEDPAFYMLKGKLYELQYRNKRDPMVAVSRRKLISVDS 180
QY 181 RSUSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIFOTOSSELKEGNNPHLL 240
DB 181 RSUSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIFOTOSSELKEGNNPHLL 240
QY 241 LLLLVIVFIPAFMSLKTNPMLRWLWKKIWA VSPERFPMPLVYKGGSGDFKKVVGAPFTGSS 300
DB 241 LLLLVIVFIPAFMSLKTNPMLRWLWKKIWA VSPERFPMPLVYKGGSGDFKKVVGAPFTGSS 300
QY 301 LELGPMSPVPSTLEVYSCHPPRSAPAKRLQLTLEQEPALVESDGVKPSFWPTAQNSSG 360
DB 301 LELGPMSPVPSTLEVYSCHPPRSAPAKRLQLTLEQEPALVESDGVKPSFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBPGLEDELLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBPGLEDELLD 420
QY 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMWGRSPGVSESEAGS 480
DB 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMWGRSPGVSESEAGS 480
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QY 481 PLAGLMDTDFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPOAS 538
RESULT 7
US-10-282-622-16
; Sequence 16, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA1 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-622-16
```

Query Match 100.0%; Score 2958; DB 4; Length 538;

Best Local Similarity 100.0%; Pred. No. 2,8e-228; Mismatches 0; Indels 0; Gaps 0;

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Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGMAAPLLLLLLLOGGMGCPDVCYTDYLOTVICILEMNNLHPSTLTLMQDOYBELKD 60
DB 1 MPRGMAAPLLLLLLLOGGMGCPDVCYTDYLOTVICILEMNNLHPSTLTLMQDOYBELKD 60
QY 61 EATSCSLHRSAHNATHATYTCMDVHFHMADIFSVNITDQSGVYSGECSFLAIESIKP 120
DB 61 EATSCSLHRSAHNATHATYTCMDVHFHMADIFSVNITDQSGVYSGECSFLAIESIKP 120
QY 121 APPNNVTFTSGQYNISWRSYEDPAFYMLKGKLYELQYRNKRDPMVAVSRRKLISVDS 180
DB 121 APPNNVTFTSGQYNISWRSYEDPAFYMLKGKLYELQYRNKRDPMVAVSRRKLISVDS 180
QY 181 RSUSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIFOTOSSELKEGNNPHLL 240
DB 181 RSUSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIFOTOSSELKEGNNPHLL 240
QY 241 LLLLVIVFIPAFMSLKTNPMLRWLWKKIWA VSPERFPMPLVYKGGSGDFKKVVGAPFTGSS 300
DB 241 LLLLVIVFIPAFMSLKTNPMLRWLWKKIWA VSPERFPMPLVYKGGSGDFKKVVGAPFTGSS 300
QY 301 LELGPMSPVPSTLEVYSCHPPRSAPAKRLQLTLEQEPALVESDGVKPSFWPTAQNSSG 360
DB 301 LELGPMSPVPSTLEVYSCHPPRSAPAKRLQLTLEQEPALVESDGVKPSFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBPGLEDELLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBPGLEDELLD 420
QY 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMWGRSPGVSESEAGS 480
DB 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMWGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPOAS 538
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```
RESULT 8
US-10-243-072-2
; Sequence 2, Application US/10243072
; Publication No. US20030148447A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Preenell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US2003014844/Alak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-072-2

Query Match      100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLILLLLLOGGMGCPDLVCYTDYLOTVICILEMNLHPSLTLLTMOQDYEBLKD 60
Db 1 MPRGMAAPLILLLLLOGGMGCPDLVCYTDYLOTVICILEMNLHPSLTLLTMOQDYEBLKD 60
QY 61 EATSCSLHRSANHTATYTCMDVHFHMADDFSVNITDQSGVYSGECSFLLAESIKP 120
Db 61 EATSCSLHRSANHTATYTCMDVHFHMADDFSVNITDQSGVYSGECSFLLAESIKP 120
QY 121 APPNVTVTSGQYINISWRSDYEDPAFYMLKGKLYEQLQYRNKGDPMVAVSPRRKLISVDS 180
Db 121 APPNVTVTSGQYINISWRSDYEDPAFYMLKGKLYEQLQYRNKGDPMVAVSPRRKLISVDS 180
QY 181 RSVALPLERFKDSSYELQVAGPMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
Db 181 RSVALPLERFKDSSYELQVAGPMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
QY 241 LLLIVIVIFPAFMSLKTPLRLMKKIWAVSPERFPMPLKYGCSGDPFKKVVGAFTGSS 300
Db 241 LLLIVIVIFPAFMSLKTPLRLMKKIWAVSPERFPMPLKYGCSGDPFKKVVGAFTGSS 300
QY 301 LEIGPMSPEVPSSTLEVYSCHPPRSAPAKRLQUTLQEPALVESDGVKPSFPTAONSGG 360
Db 301 LEIGPMSPEVPSSTLEVYSCHPPRSAPAKRLQUTLQEPALVESDGVKPSFPTAONSGG 360
QY 361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBSPGLJEDPLD 420
Db 361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBSPGLJEDPLD 420
QY 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGCVSESEBAGS 480
Db 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGCVSESEBAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPSPSYLRQWVVIPIPLSSPGPOAS 538
Db 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPSPSYLRQWVVIPIPLSSPGPOAS 538

RESULT 9
US-10-414-186-2
; Sequence 2, Application US/10414186
; Publication No. US20030175825A1
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
```

```

; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030175825A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-414-186-2

Query Match      100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLILLLLLOGGMGCPDLVCYTDYLOTVICILEMNLHPSLTLLTMOQDYEBLKD 60
Db 1 MPRGMAAPLILLLLLOGGMGCPDLVCYTDYLOTVICILEMNLHPSLTLLTMOQDYEBLKD 60
QY 61 EATSCSLHRSANHTATYTCMDVHFHMADDFSVNITDQSGVYSGECSFLLAESIKP 120
Db 61 EATSCSLHRSANHTATYTCMDVHFHMADDFSVNITDQSGVYSGECSFLLAESIKP 120
QY 121 APPNVTVTSGQYINISWRSDYEDPAFYMLKGKLYEQLQYRNKGDPMVAVSPRRKLISVDS 180
Db 121 APPNVTVTSGQYINISWRSDYEDPAFYMLKGKLYEQLQYRNKGDPMVAVSPRRKLISVDS 180
QY 181 RSVALPLERFKDSSYELQVAGPMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
Db 181 RSVALPLERFKDSSYELQVAGPMPGSSYQGTWSEMSDPVIFQTOSEBELKEGNNPHLL 240
QY 241 LLLIVIVIFPAFMSLKTPLRLMKKIWAVSPERFPMPLKYGCSGDPFKKVVGAFTGSS 300
Db 241 LLLIVIVIFPAFMSLKTPLRLMKKIWAVSPERFPMPLKYGCSGDPFKKVVGAFTGSS 300
QY 301 LEIGPMSPEVPSSTLEVYSCHPPRSAPAKRLQUTLQEPALVESDGVKPSFPTAONSGG 360
Db 301 LEIGPMSPEVPSSTLEVYSCHPPRSAPAKRLQUTLQEPALVESDGVKPSFPTAONSGG 360
QY 361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBSPGLJEDPLD 420
Db 361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBSPGLJEDPLD 420
QY 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGCVSESEBAGS 480
Db 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGCVSESEBAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPSPSYLRQWVVIPIPLSSPGPOAS 538
Db 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPSPSYLRQWVVIPIPLSSPGPOAS 538

RESULT 10
US-10-456-780-6
; Sequence 6, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
```

;; TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
;; FILE REFERENCE: 03-08
;; CURRENT APPLICATION NUMBER: US/10/456,780
;; CURRENT FILING DATE: 2003-06-06
;; PRIOR APPLICATION NUMBER: US 60/387,127
;; PRIOR FILING DATE: 2002-06-07
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 6
;; LENGTH: 538
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-10-456-780-6

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGMAAPLLLLLLGGMGCPDLYCTDYQTVICILEMNNLHPSTLTLTWQDYEELKD 60
Db 1 MPRGMAAPLLLLLLGGMGCPDLYCTDYQTVICILEMNNLHPSTLTLTWQDYEELKD 60
QY 61 EATSCSLHRSANAHATATYTCMDVFPFMAADIFSVNITDQSGNYSQECGSFLAESIKP 120
Db 61 EATSCSLHRSANAHATATYTCMDVFPFMAADIFSVNITDQSGNYSQECGSFLAESIKP 120
QY 121 APPFNVTFTSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPMAVSPRRKLISVDS 180
Db 121 APPFNVTFTSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPMAVSPRRKLISVDS 180
QY 181 RSVSLPLERKSSYELQYRAGPMGSSYQGTWSEMSDPVITQTSBELKEGNPHLL 240
Db 181 RSVSLPLERKSSYELQYRAGPMGSSYQGTWSEMSDPVITQTSBELKEGNPHLL 240
QY 241 LLLLVIFIPAFMSLKTPLMLKMKIWA VSPERFPMPLYKCGSGDFKMWGAPFTGSS 300
Db 241 LLLLVIFIPAFMSLKTPLMLKMKIWA VSPERFPMPLYKCGSGDFKMWGAPFTGSS 300
QY 301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTELOEPAELVESDGVKPSFWPTAQNSSG 360
Db 301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTELOEPAELVESDGVKPSFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDELLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDELLD 420
QY 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
Db 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTFTDSGFVSDCSSPVCEPFTSPGDEGPPRSYLRQWVVIIPPLSSPGQAS 538
Db 481 PLAGLMDTFTDSGFVSDCSSPVCEPFTSPGDEGPPRSYLRQWVVIIPPLSSPGQAS 538
```

RESULT 11
US-10-659-684-115

;; Sequence 115, Application US/10659684
;; Publication No. US20040110932A1
;; GENERAL INFORMATION:
;; APPLICANT: Novak, Julia E.
;; APPLICANT: Presnell, Scott R.
;; APPLICANT: Sprecher, Cindy A.
;; APPLICANT: Foster, Donald C.
;; APPLICANT: Holly, Richard D.
;; APPLICANT: Grose, Jane A.
;; APPLICANT: Johnson, Janet V.
;; APPLICANT: Nelson, Andrew J.
;; APPLICANT: Dillon, Stacey R.
;; APPLICANT: Hammond, Angela K.
;; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
;; FILE REFERENCE: 99-16
;; CURRENT APPLICATION NUMBER: US/10/659,684

;; CURRENT FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: US/09/522,217
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
;; NUMBER OF SEQ ID NOS: 115
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 115
;; LENGTH: 538
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-10-659-684-115

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MPRGMAAPLLLLLLGGMGCPDLYCTDYQTVICILEMNNLHPSTLTLTWQDYEELKD 60
Db 1 MPRGMAAPLLLLLLGGMGCPDLYCTDYQTVICILEMNNLHPSTLTLTWQDYEELKD 60
QY 61 EATSCSLHRSANAHATATYTCMDVFPFMAADIFSVNITDQSGNYSQECGSFLAESIKP 120
Db 61 EATSCSLHRSANAHATATYTCMDVFPFMAADIFSVNITDQSGNYSQECGSFLAESIKP 120
QY 121 APPFNVTFTSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPMAVSPRRKLISVDS 180
Db 121 APPFNVTFTSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPMAVSPRRKLISVDS 180
QY 181 RSVSLPLERKSSYELQYRAGPMGSSYQGTWSEMSDPVITQTSBELKEGNPHLL 240
Db 181 RSVSLPLERKSSYELQYRAGPMGSSYQGTWSEMSDPVITQTSBELKEGNPHLL 240
QY 241 LLLLVIFIPAFMSLKTPLMLKMKIWA VSPERFPMPLYKCGSGDFKMWGAPFTGSS 300
Db 241 LLLLVIFIPAFMSLKTPLMLKMKIWA VSPERFPMPLYKCGSGDFKMWGAPFTGSS 300
QY 301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTELOEPAELVESDGVKPSFWPTAQNSSG 360
Db 301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTELOEPAELVESDGVKPSFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDELLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDELLD 420
QY 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
Db 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTFTDSGFVSDCSSPVCEPFTSPGDEGPPRSYLRQWVVIIPPLSSPGQAS 538
Db 481 PLAGLMDTFTDSGFVSDCSSPVCEPFTSPGDEGPPRSYLRQWVVIIPPLSSPGQAS 538
```

RESULT 12
US-10-620-169-4

;; Sequence 4, Application US/10620169
;; Publication No. US20040136954A1
;; GENERAL INFORMATION:
;; APPLICANT: Grunby, Michael J
;; APPLICANT: Wurster, Andrea
;; APPLICANT: Young, Deborah
;; APPLICANT: Collins, Mary
;; APPLICANT: Whitters, Matthew
;; TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
;; FILE REFERENCE: 22058-585
;; CURRENT APPLICATION NUMBER: US/10/620,169
;; CURRENT FILING DATE: 2003-07-15

;; PRIOR APPLICATION NUMBER: 60/396,160
;; PRIOR FILING DATE: 2002-07-15
;; PRIOR APPLICATION NUMBER: 60/403,001
;; PRIOR FILING DATE: 2002-08-12
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 538
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-620-169-4

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLULLLLLOGGMGCPDLVCTDYLOTVICILEMNNLHPSSTLTLTWQDYBELKD 60
DB 1 MPRGMAAPLULLLLLOGGMGCPDLVCTDYLOTVICILEMNNLHPSSTLTLTWQDYBELKD 60
QY 61 EATSCSLHRSANHTATYTCMDVFFHMDIFSVNITDQSGNYSOECGFFLAESIKP 120
DB 61 EATSCSLHRSANHTATYTCMDVFFHMDIFSVNITDQSGNYSOECGFFLAESIKP 120
QY 121 APPENVTVTSGQYNISWRSDDYEDPAFYMLKGKLOEYLRNRGDPMAVSPRRKLISYDS 180
DB 121 APPENVTVTSGQYNISWRSDDYEDPAFYMLKGKLOEYLRNRGDPMAVSPRRKLISYDS 180
QY 181 RSVSLPLERFKOSSYELQVRAGMPGSSYOGTWSMDPVIPTQOSEBELKEGNPHLL 240
DB 181 RSVSLPLERFKOSSYELQVRAGMPGSSYOGTWSMDPVIPTQOSEBELKEGNPHLL 240
QY 241 LLLIVIFIPAFMSLKTPLMLKTIWAVSPERFPMPLKYGSGGPFKKVGA.PFTGSS 300
DB 241 LLLIVIFIPAFMSLKTPLMLKTIWAVSPERFPMPLKYGSGGPFKKVGA.PFTGSS 300
QY 301 LEIGPMSPEVPSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVKPSFPTAONSOG 360
DB 301 LEIGPMSPEVPSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVKPSFPTAONSOG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPGLEDPDLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPGLEDPDLD 420
QY 421 AGTIVLSCGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTIVLSCGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538

RESULT 13
US-10-715-998-2
;; Sequence 2, Application US/10715998
;; Publication No. US20040204562A1
;; GENERAL INFORMATION:
;; APPLICANT: Preenell, Scott R.
;; APPLICANT: Conklin, Darrell C.
;; APPLICANT: Novak, Julia E.
;; APPLICANT: Hammond, Angela K.
;; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPPAH11
;; FILE REFERENCE: 98-55
;; CURRENT APPLICATION NUMBER: US/10/715,998
;; PRIOR FILING DATE: 2003-11-18
;; PRIOR APPLICATION NUMBER: US/10/414,186
;; PRIOR FILING DATE: 2003-04-14
;; PRIOR APPLICATION NUMBER: US/09/404,641
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546

;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
;; NUMBER OF SEQ ID NOS: 91
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 538
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-715-998-2

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLULLLLLOGGMGCPDLVCTDYLOTVICILEMNNLHPSSTLTLTWQDYBELKD 60
DB 1 MPRGMAAPLULLLLLOGGMGCPDLVCTDYLOTVICILEMNNLHPSSTLTLTWQDYBELKD 60
QY 61 EATSCSLHRSANHTATYTCMDVFFHMDIFSVNITDQSGNYSOECGFFLAESIKP 120
DB 61 EATSCSLHRSANHTATYTCMDVFFHMDIFSVNITDQSGNYSOECGFFLAESIKP 120
QY 121 APPENVTVTSGQYNISWRSDDYEDPAFYMLKGKLOEYLRNRGDPMAVSPRRKLISYDS 180
DB 121 APPENVTVTSGQYNISWRSDDYEDPAFYMLKGKLOEYLRNRGDPMAVSPRRKLISYDS 180
QY 181 RSVSLPLERFKOSSYELQVRAGMPGSSYOGTWSMDPVIPTQOSEBELKEGNPHLL 240
DB 181 RSVSLPLERFKOSSYELQVRAGMPGSSYOGTWSMDPVIPTQOSEBELKEGNPHLL 240
QY 241 LLLIVIFIPAFMSLKTPLMLKTIWAVSPERFPMPLKYGSGGPFKKVGA.PFTGSS 300
DB 241 LLLIVIFIPAFMSLKTPLMLKTIWAVSPERFPMPLKYGSGGPFKKVGA.PFTGSS 300
QY 301 LEIGPMSPEVPSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVKPSFPTAONSOG 360
DB 301 LEIGPMSPEVPSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVKPSFPTAONSOG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPGLEDPDLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPGLEDPDLD 420
QY 421 AGTIVLSCGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTIVLSCGCVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538

RESULT 14
US-10-872-087-2
;; Sequence 2, Application US/10872087
;; Publication No. US20040235743A1
;; GENERAL INFORMATION:
;; APPLICANT: Sprecher, Cindy A.
;; APPLICANT: Novak, Julia E.
;; APPLICANT: West, James W.
;; APPLICANT: Holli, Richard D.
;; APPLICANT: Nelson, Andrew J.
;; TITLE OF INVENTION: SOLUBLE ZAPPAH11 CYTOKINE RECEPTORS
;; FILE REFERENCE: 00-22D1
;; CURRENT APPLICATION NUMBER: US/10/872,087
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: US 60/194,731
;; PRIOR FILING DATE: 2000-04-05
;; PRIOR APPLICATION NUMBER: US 60/222,121
;; PRIOR FILING DATE: 2000-07-28
;; PRIOR APPLICATION NUMBER: US 09/825,561
;; PRIOR FILING DATE: 2001-04-03
;; NUMBER OF SEQ ID NOS: 86

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 538

TYPE: PRT

ORGANISM: Homo sapiens

US-10-872-087-2

Query Match 100.0%; Score 2958; DB 5; Length 538;

Best Local Similarity 100.0%; Pred. No. 2,8e-228; Indels 0; Gaps 0;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MPRGMAAPLLLLLLLOGMGCPDLVCTDYQTYICILEMNNLHPSTLTLMQDQYEBLKD 60
DB 1 MPRGMAAPLLLLLLLOGMGCPDLVCTDYQTYICILEMNNLHPSTLTLMQDQYEBLKD 60
QY 61 EATSCSLHRSANHTATYTCMDVPHFMADIFSVNITDQSGNYSQECGSFLAESIKP 120
DB 61 EATSCSLHRSANHTATYTCMDVPHFMADIFSVNITDQSGNYSQECGSFLAESIKP 120
QY 121 APPNNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
DB 121 APPNNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
QY 181 RSVSLPLLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNNPHLL 240
DB 181 RSVSLPLLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNNPHLL 240
QY 241 LLLLVIFIPAFWMLKTHPLMLKTIWAVSPERFPMPLKYKCSGDFKKWVGAFTGSS 300
DB 241 LLLLVIFIPAFWMLKTHPLMLKTIWAVSPERFPMPLKYKCSGDFKKWVGAFTGSS 300
QY 301 LELGPMSPPEVSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVPKSPFWPTAONSGG 360
DB 301 LELGPMSPPEVSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVPKSPFWPTAONSGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
QY 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
DB 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPPLSSPGPOAS 538

RESULT 15
US-10-787-442-115
; Sequence 115, Application US/10787442
; Publication No. US2004026005A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/787,442
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
```

PRIOR APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 115

LENGTH: 538

TYPE: PRT

ORGANISM: Homo sapiens

US-10-787-442-115

Query Match 100.0%; Score 2958; DB 5; Length 538;

Best Local Similarity 100.0%; Pred. No. 2,8e-228; Indels 0; Gaps 0;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGMAAPLLLLLLLOGMGCPDLVCTDYQTYICILEMNNLHPSTLTLMQDQYEBLKD 60
DB 1 MPRGMAAPLLLLLLLOGMGCPDLVCTDYQTYICILEMNNLHPSTLTLMQDQYEBLKD 60
QY 61 EATSCSLHRSANHTATYTCMDVPHFMADIFSVNITDQSGNYSQECGSFLAESIKP 120
DB 61 EATSCSLHRSANHTATYTCMDVPHFMADIFSVNITDQSGNYSQECGSFLAESIKP 120
QY 121 APPNNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
DB 121 APPNNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
QY 181 RSVSLPLLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNNPHLL 240
DB 181 RSVSLPLLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNNPHLL 240
QY 241 LLLLVIFIPAFWMLKTHPLMLKTIWAVSPERFPMPLKYKCSGDFKKWVGAFTGSS 300
DB 241 LLLLVIFIPAFWMLKTHPLMLKTIWAVSPERFPMPLKYKCSGDFKKWVGAFTGSS 300
QY 301 LELGPMSPPEVSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVPKSPFWPTAONSGG 360
DB 301 LELGPMSPPEVSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVPKSPFWPTAONSGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
QY 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
DB 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPPLSSPGPOAS 538
```

Search completed: September 7, 2006, 12:57:58
Job time : 197.717 secs

QY	301	LELGWMSPEVSTLEVYSCHPSPSPAKKRLQTEHLOSPAEELVESDGYPKPSFWMTAQNSSG	360
Db	301	LELGWMSPEVPSTLEVYSCHPSPSPAKKRLQTEHLOSPAEELVESDGYPKPSFWMTAQNSSG	360
QY	361	SAYSEERDRPYGLVSIIDYTVTLDAEGRPCPCMCEDEDDGYPALDLDAIGLESPGLEBPLLD	420
Db	361	SAYSEERDRPYGLVSIIDYTVTLDAEGRPCPCMCEDEDDGYPALDLDAIGLESPGLEBPLLD	420
QY	421	AGTTVLSCGCVSAGSPGLCGPLGSLDLRLKPLADGEDMAGGLPMWGRSPGVYSESEAGS	480
Db	421	AGTTVLSCGCVSAGSPGLCGPLGSLDLRLKPLADGEDMAGGLPMWGRSPGVYSESEAGS	480
QY	481	PLAGIDMTDFSDGPFVSGDCSSPEECDFTSRGDEGRPRSYLRQMWVLPPLPLSSGPQAS	538
Db	481	PLAGIDMTDFSDGPFVSGDCSSPEECDFTSRGDEGRPRSYLRQMWVLPPLPLSSGPQAS	538

```

RESULT 2
US-10-669-920-305
; Sequence 305, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-305

```

Query Match	99.3%	Score 2938	DB 6	Length 536
Beet Local Similarity	99.6%	Pred. No. 7,2e-230		
Matches	536	Conservative	0	Mismatches 0; Indels 2; Gaps 1;
Qy	1	MPRGAAALLLLLLLQGGWGCBDLYCYTYTYLQVVICILEMMNLHPSTLLTWQDYEBLKD	60	
Db	1	MPRGAAALLLLLLLQGGWGCBDLYCYTYLQVVICI--MMNLHPSTLLTWQDYEBLKD	58	
Qy	61	EATSSLSLRSAANHATYTCMDYVFHMADDIFSVNTTDSGNSOEGCSFLAESIKP	120	
Db	59	EATSSLSLRSAANHATYTCMDYVFHMADDIFSVNTTDSGNSOEGCSFLAESIKP	118	
Qy	121	APPFNVTYFSGQYNIISWRSDYEDPAFYMLKGLQYELQYRNRRGPMVAVSPARKLISYDS	180	
Db	119	APPFNVTYFSGQYNIISWRSDYEDPAFYMLKGLQYELQYRNRRGPMVAVSPARKLISYDS	178	
Qy	181	RSVSLLPLEFRDSSYELQVRGPMPSGYOCTWSEMDPVIYFOQSELEKEGNPHILL	240	
Db	179	RSVSLLPLEFRDSSYELQVRGPMPSGYOCTWSEMDPVIYFOQSELEKEGNPHILL	238	
Qy	241	LLLLVIVEIPAFWSLKTHTPLMRMKKIAVSPERFFEMPLYKGCSDGERKUNGAPEFTSS	300	

Db	239	ILLIVIVFIPARWSLKHPLMRLMKKIMAVSPERPFMWLYGCGSDGFFKMWGAPETGSS	298
Qy	301	IELGPMSPVPESTLVESGCHPRPSPAKRLQLELOEPAVLVEDGVPKPSFWMTAONSG	366
Db	299	IELGPMSEVPSTLEVLSCHPRPSPAKRLQLELOEPAVLVEDGVPKPSFWMTAONSG	358
Qy	361	SAYSEERDRPYGLVSIDVTYVLDAGPCTMPCSCEDDGYPALDLDAGLEBSPGLEDPPLD	420
Db	359	SAYSEERDRPYGLVIDTYVLDAGPCTMPCSCEDDGYPALDLDAGLEBSPGLEDPPLD	418
Qy	421	AGTTVLSGCCVAGSPGLGGLPLSLDLRLKPLADEDAWAGGLPMWGRSPGVSESEAGS	480
Db	419	AGTTVLSGCCVAGSPGLGGLPLSLDLRLKPLADEDAWAGGLPMWGRSPGVSESEAGS	478
Qy	481	PLAGLDMDTFDSGPFVSGDCSSPVECDFPSGCBGPPRSTLRLQWVYLPPLSSGPAS	538
Db	479	PLAGLDMDTFDSGPFVSGDCSSPVECDFPSGCBGPPRSTLRLQWVYLPPLSSGPAS	536

```

/ RESULT 3
/ US-10-669-920-307
/ Sequence 307, Application US/10669920
/ Publication No. US20060194265A1
/ GENERAL INFORMATION:
/ APPLICANT: Moritz, David W.
/ APPLICANT: Malandro, Marc S.
/ TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
/ FILE REFERENCE: 20366-066001
/ CURRENT APPLICATION NUMBER: US/10/669,920
/ CURRENT FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: US 10/004,113
/ PRIOR FILING DATE: 2001-10-23
/ PRIOR APPLICATION NUMBER: US 10/052,482
/ PRIOR FILING DATE: 2001-11-08
/ PRIOR APPLICATION NUMBER: US 09/997,722
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: US 10/034,650
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: US 10/085,117
/ PRIOR FILING DATE: 2002-02-27
/ PRIOR APPLICATION NUMBER: US 10/087,192
/ PRIOR FILING DATE: 2002-03-01
/ PRIOR APPLICATION NUMBER: US 10/322,281
/ PRIOR FILING DATE: 2002-12-17
/ PRIOR APPLICATION NUMBER: US 10/322,696
/ PRIOR FILING DATE: 2002-12-17
/ NUMBER OF SEQ ID NOS: 1441
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 307
/ LENGTH: 536
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-669-920-307

```

Query Match	Similarity	Score	DB	Length
Beet	99.3%	2938	6	536
Local	99.6%	Pred. No. 7,2e-230		
Matches	536	Conservative	0	Mismatches 0; Indels 2; Gaps 1
QY	1	MPRGMAAPLLLLLLLGGGNGCPDLVACYTDYDTVTVCILEMNNLHPSTLTLTMODQYEELKD	60	
DB	1	MPRGMAAPLLLLLLLGGGNGCPDLVACYTDYDTVTVCII--MNNLHPSTLTLTMODQYEELKD	58	
QY	61	EATSCSLRSAAHNAHTATYTTCMDVFHRMADDFSVNITDQSGNVSGECSGFFLLAESIKP	120	
DB	59	EATSCSLRSAAHNAHTATYTTCMDVFHRMADDFSVNITDQSGNVSGECSGFFLLAESIKP	118	
QY	121	APPFVNTYTESGGVNIISWRSDYEDPAFPLMGKIQLEYELQVNRBGPMAVSRRLKISVDS	180	
DB	119	APPFVNTYTESGGVNIISWRSDYEDPAFPLMGKIQLEYELQVNNRBDPMVAISRRLKISVDS	178	
QY	181	RSVSLILPLEFRKDSSEYELQVAPGPGSSVQGTWSEWSDPVITFOTQSEELKEGNNPHILL	240	

Db 179 RSVSLPLPERKDSSEYELQVRAGPMPGSSYQGTWSEMSDVIPTQSEELKEGMNPHLL 238
Qy 241 LLLLVVVFPAFMSLKTHPMLRMKTIWAPSPERFPMPLTKGCGSGFKKWCAPFGSS 300
Db 239 LLLLVVVFPAFMSLKTHPMLRMKTIWAPSPERFPMPLTKGCGSGFKKWCAPFGSS 298
Qy 301 LELGPMSPVSTLEYVSCHPSPSPAKRLQTELOEPAELVESDGVKPSFMPFTAQNSG 360
Db 299 LELGPMSPVSTLEYVSCHPSPSPAKRLQTELOEPAELVESDGVKPSFMPFTAQNSG 358
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPSGLIEDLLD 420
Db 359 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPSGLIEDLLD 418
Qy 421 AGTTVASCVCVSGSPGLGPGSLDLRLKPLADGDMAAGLPMGGRSGCVSEBAGS 480
Db 419 AGTTVASCVCVSGSPGLGPGSLDLRLKPLADGDMAAGLPMGGRSGCVSEBAGS 478
Qy 481 PLAGLMDTFDSCGVSGSDCSSPVCECDFTSPGDEGPPRSYLROWVVIPLPLSPGQAS 538
Db 479 PLAGLMDTFDSCGVSGSDCSSPVCECDFTSPGDEGPPRSYLROWVVIPLPLSPGQAS 536

RESULT 4

US-10-806-611-8
Sequence 8, Application US/10806611
Publication No. US20060159655A1
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chiu, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING ACONISTS OF
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806, 611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456, 920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent version 3.2
SEQ ID NO 8
LENGTH: 529
TYPE: PRT
ORGANISM: Mus musculus
US-10-806-611-8

Query Match 58.7%; Score 1735.5; DB 6; Length 529;

Best Local Similarity 62.7%; Pred. No. 1.6e-132; Indels 17; Gaps 6;
Matches 340; Conservative 49; Mismatches 136;

Qy 1 MPRGMAAPLILLLOGMGCPDLVCYTDYQTVICILEMNNLHPSTLTLTMODQYBELKD 60
Db 1 MPRGPAVALILLIHGMSCLDLCTCYDYLMTITCVLETSPSPSILSLTMODEYBELQD 60
Qy 61 EATSCSLHRSANAHATATYTCMDVFHFMADDIFSVNITDQSGNYSQECGSFLAIESIKP 120
Db 61 QETFCSLHRSAGHTTHIWTCHMRLSQFLSDEVIIVVTTDQSGNNSQECGSFVLAIESIKP 120
Qy 121 APPENVTVTSSGQYNISWBSDEDPAPFYMKGKLYELOVRNRGDPMAVSPRKLISVDS 180
Db 121 APPENVTVTSSGQYNISWBSDEDPAPFYMKGKLYELOVRNRGDPMAVSPRKLISVDS 180
Qy 121 APPENVTVTSSGQYNISWBSDEDPAPFYMKGKLYELOVRNRGDPMAVSPRKLISVDS 180
Db 121 APPENVTVTSSGQYNISWBSDEDPAPFYMKGKLYELOVRNRGDPMAVSPRKLISVDS 180
Qy 181 RSVSLPLPERKDSSEYELQVRAGPMPGSSYQGTWSEMSDVIPTQSEELKEGMNPHLL 240
Db 181 RSVSLPLPERKDSSEYELQVRAGPMPGSSYQGTWSEMSDVIPTQSEELKEGMNPHLL 240
Qy 241 LLLLVVVFPAFMSLKTHPMLRMKTIWAPSPERFPMPLTKGCGSGFKKWCAPFGSS 299
Db 241 LLLLVVVFPAFMSLKTHPMLRMKTIWAPSPERFPMPLTKGCGSGFKKWCAPFGSS 299
Qy 300 SLELGPMSPVSTLEYVSCHPSPSPAKRLQTELOEPAELVESDGVKPSFMPFTAQNSG 356
Db 300 SLELGPMSPVSTLEYVSCHPSPSPAKRLQTELOEPAELVESDGVKPSFMPFTAQNSG 356

Db 300 SLELVQSSITTSAL-----HSLYPAKEKKEPGLGLEOLECDGMSPEGHMCITPLAA 354
Qy 357 NSGSAVSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPSGLIED 416
Db 355 GQAVSAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPSGLIED 414
Qy 417 PLIDACTVASCVCVSGSPGLGPGSLDLRLKPLADGEDMAAGLPMGGRSGCVSEBAGS 476
Db 415 LLLVTPPAFLSCGCVSGSGSLRLGSGPSGLDLRLKPLADGEDMAAGLPMGGRSGCVSEBAGS 474
Qy 477 EAGSP-PLGMDTFDSCGVSGSDCSSPVCECDFTSPGDEGPPRSYLROWVVIPLPLSPGQAS 536
Db 475 EAGSP-PLGMDTFDSCGVSGSDCSSPVCECDFTSPGDEGPPRSYLROWVVIPLPLSPGQAS 527
Qy 537 AS 538
Db 528 SS 529

RESULT 5

US-10-669-920-302
Sequence 302, Application US/10669920
Publication No. US20060194265A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Melandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 20366-066001
CURRENT APPLICATION NUMBER: US/10/669, 920
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 302
LENGTH: 579
TYPE: PRT
ORGANISM: Mus musculus
US-10-669-920-302

Query Match 58.7%; Score 1735.5; DB 6; Length 579;

Best Local Similarity 62.7%; Pred. No. 1.6e-132; Indels 17; Gaps 6;
Matches 340; Conservative 49; Mismatches 136;

Qy 1 MPRGMAAPLILLLOGMGCPDLVCYTDYQTVICILEMNNLHPSTLTLTMODQYBELKD 60
Db 1 MPRGPAVALILLIHGMSCLDLCTCYDYLMTITCVLETSPSPSILSLTMODEYBELQD 110
Qy 61 EATSCSLHRSANAHATATYTCMDVFHFMADDIFSVNITDQSGNYSQECGSFLAIESIKP 120
Db 61 QETFCSLHRSAGHTTHIWTCHMRLSQFLSDEVIIVVTTDQSGNNSQECGSFVLAIESIKP 170
Qy 121 APPENVTVTSSGQYNISWBSDEDPAPFYMKGKLYELOVRNRGDPMAVSPRKLISVDS 180
Db 121 APPENVTVTSSGQYNISWBSDEDPAPFYMKGKLYELOVRNRGDPMAVSPRKLISVDS 230
Qy 171 APPENVTVTSSGQYNISWBSDEDPAPFYMKGKLYELOVRNRGDPMAVSPRKLISVDS 230
Db 171 APPENVTVTSSGQYNISWBSDEDPAPFYMKGKLYELOVRNRGDPMAVSPRKLISVDS 230
Qy 181 RSVSLPLPERKDSSEYELQVRAGPMPGSSYQGTWSEMSDVIPTQSEELKEGMNPHLL 240
Db 181 RSVSLPLPERKDSSEYELQVRAGPMPGSSYQGTWSEMSDVIPTQSEELKEGMNPHLL 240
Qy 231 RSVSLPLPERKDSSEYELQVRAGPMPGSSYQGTWSEMSDVIPTQSEELKEGMNPHLL 290
Db 231 RSVSLPLPERKDSSEYELQVRAGPMPGSSYQGTWSEMSDVIPTQSEELKEGMNPHLL 290

Qy 241 LLLVIVIPAFMSLKTPLRLMKIWA-VSPERFEMPLYKGCSDGDFKKWGAFFG 299
Db 291 LLAVALIIVL-VFMGLKTHLPRLMKIWAIPVTPESFPQIYRHSNGFKMVTPTFAS 349
Qy 300 SLBGLPMSPEVPTLVEVYSCHPSPAKRQLTELOEPAELVESDGVKPSFW---PTAQ 356
Db 350 SIELVPSSTTSMAL-----HLSTLYPAKEKKFPGLPGLAEQLECDGMEPECHWCIPLAA 404
Qy 357 NSGSAVSEERDRYGLVSTIVTVVLDAGECTPCCSEDDGYPALDLDALESFGLD 416
Db 405 GQAVASVSEERDRYGLVSTIVTVVGDABGLCVWPCSCEDDGYPAMNLDAGRESGPNSED 464
Qy 417 PLDAGTTVSCGCVSAGSPGLGSLDLRLKPLADGEDWAGLPMWGRSPGVSES 476
Db 465 LLLVTDPAFLSCGCVSAGSLRGLSGSLDLRLKSLFAKEDWTDADPTWRGSGSGSES 524
Qy 477 EAGSPLAGLMDTPDSCGCVSAGSPVECDFTSPGDEGPPRSYLROWVVIPLPLSPQ 536
Db 525 EAGSP-PGLMDTDTDSGFGAGSDGSPVET-----DEGPPRSYLROWVVIPLPLSPQ 577
Qy 537 AS 538
Db 578 SS 579

RESULT 6
US-10-669-920-285
; Sequence 285, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-285

Query Match 9.6%; Score 284; DB 6; Length 549;
Best Local Similarity 26.1%; Pred. No. 5.6e-15;
Matches 137; Conservative 73; Mismatches 201; Indels 114; Gaps 30;

Qy 5 WAAPLPLLL--LQGM-----GCPDLYCYTDYLGQVYICLEMNHLHPSTLTLTWQOYE 56
Db 8 WRPLPLLLPLATSMASAAVNGTSQFTCFYNSRANISCV---WS-----ODG 52
Qy 57 ELKDEATSCSLH-----RSANAT-----HATYTCM-----DVHFMAADIFSUNITD 100
Db 53 ALQD--TSCQVHAMPRDRRMNQCTCELLPVSGASWACNLLIGAPDSQKLTVTYDITLVLYLC 110

Qy 101 QSGNYSQECG--GFLAESIKPAPFENVTVTFSGQVYINISRSYEDBAPFMYLKGLOVEL 158
Db 111 REGVRRMVAALIQFKEPENTRLMAPISLQVHVETCNISWEI---SQASHYFERHLEFEA 167
Qy 159 QYRNRGDPMAVSPARKLISVDSRSVSLPLLEFRKDSSEYELQVAGPMPGSSYOGTSEMS 218
Db 168 RTLSPGHTWEAP---LLTLKQKQEWICLETLLTPDTYERQVYKVPLOGEF---TTWSPWS 222
Qy 219 DPAVFORQSEBELKRG---WNPPLLLLIVIVFIPAFMSL-----KTHPLRLW-KKIWA- 269
Db 223 QPLAFRTKPAALGKDTTPWLGHLVLGSGAFGIIIVYLINCRNTP-----MLKVLKC 278
Qy 270 -VSPERFEMPLYKGCSDGDFKKWGAFFGSSLELGWSPDEVSTLEVYSCHPSPAKR 328
Db 279 NTPDPSKFFSQLSBHGDDVQXWLSFPSSSPGLABEL-SPLEV-----LER 328
Qy 329 LQTELOEPALVESDGVKPSFMPPTAQNCGSAYSEERDRYGLVSTIVTVVLDAGEPC 388
Db 329 DKVTQL-----LLQDKVPEPA-----SLSNHSLTSCFTYQGYFFPLPDALIEIA---C 376
Qy 389 -----TWPCSEDD-----GYPALDDAGLEPSPGLEDPLDAGTTVLSGCVSAGSPG- 437
Db 377 QVYFTYDPIYSEEDPDGSAAPGTPGSPQPLQPSG-BD---DAYCTFSPSDLLILFSPSL 432
Qy 438 LGGP-----LGSILDLRLKPLAD--GEDWAGLPMWGRSPG 471
Db 433 LGGPSPSTAPGSGGAGEERMPSLQERVRDW-DPQPLGPPPTPG 476

RESULT 7
US-10-669-920-287
; Sequence 287, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 287
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-287

Query Match 9.6%; Score 284; DB 6; Length 549;
Best Local Similarity 26.1%; Pred. No. 5.6e-15;
Matches 137; Conservative 73; Mismatches 201; Indels 114; Gaps 30;

Qy 5 WAAPLPLLL--LQGM-----GCPDLYCYTDYLGQVYICLEMNHLHPSTLTLTWQOYE 56
Db 8 WRPLPLLLPLATSMASAAVNGTSQFTCFYNSRANISCV---WS-----ODG 52
Qy 57 ELKDEATSCSLH-----RSANAT-----HATYTCM-----DVHFMAADIFSUNITD 100

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Db      53 ALQD--TSCOVHAMPDRRNNQTCCELLPVSOASMACNLLIAGPDSOKLTTVDITLAVLC 110
Qy      101 QSGNYSQECG--SEFLAESIKRPAPFNVVTVFSGQYNIISMSRDEYEDAPFYLKGLQYEL 158
Db      111 REGVRMRVMAIQDPKPEPNIILMAPISLQVHVETCNIISWEI---SQASHYFERHLEFEA 167
Qy      159 QYRRGQPMVAVSPRRKLIISVDSRSVSLPLEFRKDSSEYLOVRAGPMGSSYQGTSEMS 218
Db      168 RTISPGHTWEAP---LTLTKQKQEWICLETITRPTDYEFQVRVKPQGER--TTWSPWS 222
Qy      219 DVIYFQOSEELKEG---WNPDLILLLVIVFIPAFMSL---KTHPLRLM--KXIMA- 269
Db      223 QPLAFKRPALGKDTITPMIGHLVLVSGARGFIIIVLLINCNTGP---WLKXVLC 278
Qy      270 -VSPERPFMPLYKSGSGDFPKKVGAPFTGSSLELGWSPBPSTLEVYSGHPPRSPAKR 328
Db      279 NTPDPSKFFSGLSEHGVDVQKWLSPSSPSSPSSPGLAPEI-SPLEV-----LER 328
Qy      329 LQUTLEOPALVESDGVPRKPSFWPTQNSGSAVSEBRPGLVSLDITVTLDAAGPC 388
Db      329 DKYVQL-----LQQDKVPEPA---SLSSNHSILTSCFTQGYFFPHLPDALEIEA---C 376
Qy      389 -----TWPCGEDD-----GYPALDLDAGLEPSPGLEPDLDACTVLSGCVSAGSPG- 437
Db      377 QVYFTYPIYSEEDDEGVAGAFPTGSSPOLOPLSG-ED---DAYCTPSSRDDLLFSPSL 432
Qy      438 LGGP-----LGSLLDLRLKPLAD--GEDMAGLPMWGRSPG 471
Db      433 LGGSPSPSTAPGSGAGEBRNPFSLQGRVPRDW-DPQPLGPRPG 476

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RESULT 8
US-10-659-920-280
; Sequence 280, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Moritz, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004, 113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052, 482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997, 722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034, 650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085, 117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087, 192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322, 281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322, 696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FASTSEQ for windows Version 4.0
; SEQ ID NO 280
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-659-920-280

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Query Match      8.1%; Score 240.5; DB 6; Length 537;
Best Local Similarity 23.6%; Pred. No. 1.8e-11;
Matches 138; Conservative 64; Mismatches 198; Indels 185; Gaps 30;

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Qy      5 WAAPL--LILLQSGW-----GCPDLVCTDYDQYICILEMWNHLPSTLTITLWQOYE 56

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Db      8 WSLIYVELLLATPMASAAVKNOCSHLECFYNSRANVSC---MWS-HEALNV----- 56
Qy      57 ELKDEATCSGLHSAHNAATATTCMDVPH-----EMADIFSVNI 98
Db      57 -----TTCVHAKS-NLRHMNKTCELTLVROASMACNLLIGSPESQSLTSVLLINV 109
Qy      99 T--DQSGNYSQECGSEFLAESIKRPAPFNVVTVF--SGQYNIISMR-----SDYEDAPFYL 150
Db      110 VCBEKGMRRVKTCDFPFPNLRVAPHSLOVHLIDTORCNISKVSVSHYIEP----- 164
Qy      151 KGLQYELQYRRNGDPMVAVSPRRKLIISVDSRSVSLPLEFRKDSSEYLOVRAGPMGSSY 210
Db      165 --YLEFARRRLIGHSEDA---SVLSKQRQOMFLFEMLIPTSYEVQVRVKAQRNNT- 218
Qy      211 QGTWSEKSDVITQ---TQSEELKEGNPHLLILLVIVFIPAFMS----- 254
Db      219 -GTWSPWSQLTRFMADPMKEIILPMW---LRYLLVLVLCFSGFFSCVYILVKRYLGP 273
Qy      255 -----LKTHPLRLMKIIMVSPERPFMPLYKSGSGDFPKKVGAPFTGSSLELGWSPPE 309
Db      274 WLKTVLKC-----IPDSEFFSGLSOGHGDLOKWLSSPVPLSPFSPGAPPE 322
Qy      310 VPSTLEVYSGHPPRSPAKRLQUTLEOPALVESDGVPRKPSFWPTQNSGSAVSEBRDR 369
Db      323 I-SPLEVLD-----GSKAVQLL-----LQKDSAPLPS-----PSGHSQASCTNQ 363
Qy      370 PY-----GLVSDITVTLDAEGPCT-----MPCCEDDGY----- 399
Db      364 GYFFPHLPNALETIESCQVFTYDPCVBEVEEDGSRLEPSPPLPLPGLGEODDYCAFP 423
Qy      400 PALDLDAGLEPSPGLEPDLDACT-----VLSGCVSAGSPGLGAPLGLSLDLRLK 450
Db      424 PRDLL---LIFSPLSTPNTAYGSRABERSPLSLHGLPLSLASRLMK-LORPLERM- 478
Qy      451 PPLADGEDMAGLPMWGRSPGVSESEAGSP-----LAGLMD 488
Db      479 -PEGDE-----GLSANGSGQASVPEGNLHGQDD 508

```

```

RESULT 9
US-10-511-937-2426
; Sequence 2426, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Moritz, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511, 937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131, 831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325, 899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2426
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2426

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Query Match      7.2%; Score 213; DB 6; Length 508;
Best Local Similarity 21.6%; Pred. No. 2.9e-09;

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Matches 127; Conservative 63; Mismatches 175; Indels 224; Gaps 30;
QY 9 LLLLLGGGCGP-----DVCYDYDTQVTCILE--MMNLHP 44
DB 15 LCLLLAGAAWAPENLPDPKRESKALLAARGPEELCTFERLDLVCFMEEAASAGV 74
QY 45 STLTLTQDDYBELKDEATS-CSLRSANHTATYTCM--DVHFMDIPSNVITD 100
DB 75 GWSFSFIQ-----LEDEPKLCRLHQAPTAGAVRWCSPFLDTSSFP--LELVTA 126
QY 101 QSGNYSQECGFLAESIKRAPPNVTVTF-----SGQYNIWSRSD 141
DB 127 ASG-----APRYRVIHINEVLLDPAVGLVARLDESCHVLLRLMP 169
QY 142 YEDPAFMLKGLQYELQYRNRRGPMVSPRKLISVDSRSVSLPFEFRDSSYELQY 201
DB 170 PETP---MTSHIRYEDVDSAGAGSV--QRVEILEGRTECVLS-NLRGRTYTPAVR 221
QY 202 AGPMGSSYOGTSEWSDPVIPTQSEELKEGNPHLL--LTLVTVFIAPFWSLKTTP 259
DB 222 A-RMAEPSFGGFMASSEPVSLTPSD---LDPLILTLVLVLVLTVALLSHR 275
QY 260 LWRIMKKIW-AVSPERFFMPLKCGSGDFKVV---GAPFTGSSDELGFWSPVSTL 314
DB 276 R-ALKQKIWGPISPESEPEGLFTTHKGNFQMLYQNDGLM-----WSPCTPTE 325
QY 315 EYVSGHPPRPAKRLQTELOEPALVESDGVPRPSTWPTQNSGSAVSEBRPVLV 374
DB 326 D---PPAS-----LEVLSERC-----WGTWQ----- 343
QY 375 SIDTVTLDAEGPCTWCSGDDGYPALDLDALEPSPGLEPDLDAAGTVLISGCVSAG 434
DB 344 AVEGCT--DBEGPLLEPVGSEHAODTYLVLDKMLPR----- 378
QY 435 SPGLGPGLSLDRLKRPPLADGEDWAGLPGVSGRSPGVSEASGSLAGLMDTPDPSGF 494
DB 379 -----NPPSED-----LP-----GPGG-----SVDIYAMDEGS 401
QY 495 VGSDCSSPVECDFTSPGDEG-----PRSTLRQWVTP--PP 529
DB 402 EASCSGALA---SKPSPEGASAAAFXYTILDPSSQLRLPWTLCPELPP 447
RESULT 10
US-10-669-920-292
; Sequence 292, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292

LENGTH: 890
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-669-920-292
Query Match 7.2%; Score 213; DB 6; Length 890;
Best Local Similarity 20.3%; Pred. No. 5,9e-09;
Matches 112; Conservative 84; Mismatches 221; Indels 136; Gaps 24;
QY 22 DVCYDYDTQVTCILEMNN-----LHPSTLTTLWQOYBELKDEATSCSLHRS 70
DB 248 NLCCFFDGIQSLCSMWVWQTGTSVSGFLPYRSPVA-----PEKCSPVVKEP 297
QY 71 ANHATATYTCNHDVFHMDIFSVNITQSGNYSQECGFLA-ESIKRAPP-FNVTV 128
DB 298 PGASVYTRHCSLPVPEPSHISQYTSVK-----HLEQCKFTMSYNIHIGMEPTLNLTK 351
QY 129 TFGQYNIWSRSDYEDPAFMYLKGLOELQYRNRRGPMVSPRKLISVDSRSVSLPL 188
DB 352 N-RDSYSLHWETQKMAVSFI-----BHTFQYQYKKKSDMEDSKTENLDRAHSMDS- 402
QY 189 EFRKDSYELQYAGPMGSSYOGTSEWSDPVIPTQSEELKEGNPHLL--LTLVTVF 248
DB 403 QLEBDTSYCARVYKPI--SNYDGIWSKMSSEYTWKT-DWVMPETLWTLVLTFLTL 459
QY 249 IPAFWSLKTHPLRLMKKIWAVSPERFFMPLKCGSGDFKVVGAFTGSSDELGFWSP 308
DB 460 ILRPGCVSVRY--KMKK-KIRNPSKSL-----FQDGKGLWP--- 495
QY 309 EVPSTLEVSCHBP--RSPAKRLQTELOEPALVESDGVKPSFWPTAONSGSAYSEE 366
DB 496 --PGSMAAFATKQPALQCPGSRLLAEQQ-----GESYVHL 528
QY 367 RDRPYGLVSTIDTYVL--DAEGCTWPCSCED--DGYPALDLDALEPSPGLEPDL 422
DB 529 EDNVSPLETLIEDNIIRVPPSGPDYTPAASSTEQLPNVQVGEPPNRRKOLPSPD-- 586
QY 423 TVYLSGCVSAGSPGLGCP---LGSLLDRLKRPPLADGE---PWAGLPGVSGRSPG- 472
DB 587 -----FNGPYLGPPOSHLPDLPDQSGPQVGSGLKRALPGSLFETWCLPFGQAO 636
QY 473 -----VSESEAGSPLAGLMDTPDPSGFVGSDCSSPVECDFTSPGDEGPRSTLRQWV 525
DB 637 LVPLSQVMGQGMNDVCGSSLETSFGSPVPEKPNPEVLEMSBEQEARNDP----- 687
QY 526 IPPPLSSPGQAS 538
DB 688 VTLPISSGPGE 700
RESULT 11
US-10-669-920-297
; Sequence 297, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 297
LENGTH: 895
TYPE: PRT
ORGANISM: Homo sapiens
US-10-669-920-297

Query Match 7.0%; Score 206; DB 6; Length 895;
Best Local Similarity 22.9%; Pred. No. 2.2e-08;
Matches 142; Conservative 66; Mismatches 225; Indels 188; Gaps 31;

22 DLVCYTDYLQTVICILEMMNLHPSTLT-LTWODQYBELKDEATSC-----SLHRSAH-72
245 NLECFPGGAVALSCSWEVRKEVASVSFGLFYKSPDAGEECSPVLRGLSLHTRHHC-304
73 -----NATATYTCMDVHFPMADIFSVNITQSGNYSQECGSLIAESIKAPPPNV-126
305 QIPVDDPATHGQY-----IVSV-----QPRRAEKHKS---SVNIQMAPP-SL-343
127 TVTFSG-QYNISW-----RSDYEDPAFYMLKGKLOLEYQYNNRGDPMVSPRRKLISVDS-180
344 NVTKDGSYSLRMTMKRYEHIDHTF-----EIQYKDKATWDSKTETL--QNA-392
181 RVSILPLERKDSYELQVAGPMPGSSYQGTSEMSDPVIFQTOSEBELKEGNPHLL-240
393 HSMALPALLE--PSTRYMARVY-RTSRTGYNGIMSEMSSEARSWDTES--VLPWVIALIV-447
241 LLLLVIVFIP-AFMSLKTPLMLRMKIMAVSPERFPMPLKKGSGDFKMW---VGAP-295
448 IFLTIAVLALRFGIGYRLRRKWEKIPNPSKSHLFQ-----NGSAELMPGSMGAF-501
296 FTGSLLEGPWS---PEV-----PSTLE--VYSGHPPRPAKRLQUTLEOE-336
502 TSGSPHOGPMGSRFPBLEGVFPVGFDSSEVSPLTIEDPKHVCDDPPSGDPTTPAASDLPT-561
337 PAELVESDGVKPSFPMPTAONGSGSAYSEERDRPYGLVSDTVTLDAEGCTWP---CS-393
562 EQPSPQGPAPPAHTEKQASS-----FDNNGYILGPPHRS-599
394 CEDD-GYPALDLDAGLEBSP---GLEBDPLDAGTTVSLSCGVASGSPGLG-----G-440
600 LPDILGQPEPQEGSQSPPGSLLEYLCLPAGQOVQVLPQAQMGQOAVEVERRPSQG-659
441 PLGSLDLRLKPLADGEDMAGGLPMGGRSP-----GVSESEAGSLAGLMDPTPSG-493
660 AAGS-----PSLES-----GGAPPALGPRVGGQDQKOSPVAIPMSGDTEDPG-704
494 FVGSDCSPVECDFT-----SPGDEGPPRSYLQ-522
705 -VASGYVSSADLVTPMNSGASSVSLVPSLGLPDSQTPSLCPGLASGPGAGPVKSGREG-763
QY 523 WVVIIP-----PLSSPGP-535
DB 764 YVELPPIEGSRPSRPNPNVP-784

RESULT 12
US-10-669-920-299
Sequence 299, Application US/10669920
Publication No. US20060194265A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 20366-066001
CURRENT APPLICATION NUMBER: US/10/669,920
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113

PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 299
LENGTH: 895
TYPE: PRT
ORGANISM: Homo sapiens
US-10-669-920-299

Query Match 7.0%; Score 206; DB 6; Length 895;
Best Local Similarity 22.9%; Pred. No. 2.2e-08;
Matches 142; Conservative 66; Mismatches 225; Indels 188; Gaps 31;

22 DLVCYTDYLQTVICILEMMNLHPSTLT-LTWODQYBELKDEATSC-----SLHRSAH-72
245 NLECFPGGAVALSCSWEVRKEVASVSFGLFYKSPDAGEECSPVLRGLSLHTRHHC-304
73 -----NATATYTCMDVHFPMADIFSVNITQSGNYSQECGSLIAESIKAPPPNV-126
305 QIPVDDPATHGQY-----IVSV-----QPRRAEKHKS---SVNIQMAPP-SL-343
127 TVTFSG-QYNISW-----RSDYEDPAFYMLKGKLOLEYQYNNRGDPMVSPRRKLISVDS-180
344 NVTKDGSYSLRMTMKRYEHIDHTF-----EIQYKDKATWDSKTETL--QNA-392
181 RVSILPLERKDSYELQVAGPMPGSSYQGTSEMSDPVIFQTOSEBELKEGNPHLL-240
393 HSMALPALLE--PSTRYMARVY-RTSRTGYNGIMSEMSSEARSWDTES--VLPWVIALIV-447
241 LLLLVIVFIP-AFMSLKTPLMLRMKIMAVSPERFPMPLKKGSGDFKMW---VGAP-295
448 IFLTIAVLALRFGIGYRLRRKWEKIPNPSKSHLFQ-----NGSAELMPGSMGAF-501
296 FTGSLLEGPWS---PEV-----PSTLE--VYSGHPPRPAKRLQUTLEOE-336
502 TSGSPHOGPMGSRFPBLEGVFPVGFDSSEVSPLTIEDPKHVCDDPPSGDPTTPAASDLPT-561
337 PAELVESDGVKPSFPMPTAONGSGSAYSEERDRPYGLVSDTVTLDAEGCTWP---CS-393
562 EQPSPQGPAPPAHTEKQASS-----FDNNGYILGPPHRS-599
394 CEDD-GYPALDLDAGLEBSP---GLEBDPLDAGTTVSLSCGVASGSPGLG-----G-440
600 LPDILGQPEPQEGSQSPPGSLLEYLCLPAGQOVQVLPQAQMGQOAVEVERRPSQG-659
441 PLGSLDLRLKPLADGEDMAGGLPMGGRSP-----GVSESEAGSLAGLMDPTPSG-493
660 AAGS-----PSLES-----GGAPPALGPRVGGQDQKOSPVAIPMSGDTEDPG-704
494 FVGSDCSPVECDFT-----SPGDEGPPRSYLQ-522
705 -VASGYVSSADLVTPMNSGASSVSLVPSLGLPDSQTPSLCPGLASGPGAGPVKSGREG-763
QY 523 WVVIIP-----PLSSPGP-535
DB 764 YVELPPIEGSRPSRPNPNVP-784

RESULT 13

US-10-669-920-295
; Sequence 295, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004, 113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052, 482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997, 722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034, 650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085, 117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087, 192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322, 281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322, 696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 901
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-295

Query Match 6.9%; Score 204.5; DB 6; Length 901;
Best Local Similarity 23.7%; Pred. No. 2.9e-08;
Matches 121; Conservative 51; Mismatches 166; Indels 153; Gaps 25;

QY 117 SIKAPPNNVTYTSQ-QYNISW-----RSYEDPAFMYLKGLOLYQYNNRQDPNAYS 170
DB 341 NIDAMP-SLNVTDGDSYSLRMETMKRYEIDHTF-----EIYKQOTATWDS 390
QY 171 PRRLISVDSRSVSLPLEFRKSSYELQVAPGMPGSSYQGTSEMSDPVIFOTOSHEL 230
DB 391 KTEL--QNASMLPALE--PSTRYMARVAV-RTSRTGYNGTISENSEASNDTES--V 443
QY 231 KEGNPHLLLLLVIVFIP-AFWSLKTHPMLRMKIMAVSPDERFMPLYKGCSDGDFK 289
DB 444 LPMWVLLIVIFLTIIVLLALRFGCIYGRRLRRKWEKIRPNPSKSHLFQ-----NSGAE 497
QY 290 KW----VGAPFTGSLLEGWSS--PEV-----PSTLE--VTSCHPSPSPA 326
DB 498 LMPGMSAFTSGSPPHQPGWGSRRFPELEGVPVGFGESEVSPLTIBDPKIVCDPSPGPD 557
QY 327 KRLQLTQELQEPALVESDGVKPSFMPPTAONSGGSAVSEERDRPYGLVSIIDTVTLDAEG 386
DB 558 TTPASDLPTREQPSPQPGPPASHTEPKQAS-----PDPNG 595
QY 387 PCTWP---CSCCEDD-GYPALDLDALEBSP---GLEPDLDACTTVLSGCVSAGSPGLG 439
DB 596 PYLGPHSRSLPDLIGPPEPQEGSGQKSPPGSLLEYLCLPAGGOVQLVPLAQMGPGQA 655
QY 440 -----PRLGLDLRLKPLPLADGEDMAGGLWGGRRSP-----GGVSESGAGSLA 483
DB 656 VEVERRDSQGAAGS-----PSLESG-----GGAPALGPRVGGDQKDSPPVAIP 700
QY 484 GLMDTDFSGFVSGDCSSPVECDFT-----SRGD 512
DB 701 MSSGDTIDPG-VASGYVSSADLVFTPNSGASSVLSGLPSDQTSBLCGLASGPPGA 759
QY 513 EGPRSYLRQWVVIIP-----PLSSPGP 535
DB 760 PGFVKSQFEGVELPPIEGRSFRSPRNVP 750

RESULT 14
US-10-505-928-650
; Sequence 650, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505, 928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363, 019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 650
; LENGTH: 825
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-650

Query Match 6.5%; Score 193.5; DB 6; Length 825;
Best Local Similarity 21.8%; Pred. No. 2e-07;
Matches 161; Conservative 69; Mismatches 220; Indels 289; Gaps 42;

QY 17 GWCGRDLY-----CYTDVLOTVICILEMWNLHPST-----L 47
DB 2 GMLCSGLLPVSCCLVLLQVASSGNMKVLOEPTVSDVMSISTC---EKKNGPTNCSTEL 58
QY 48 TLTWQDYBELKDEATSCSLHRSANHTATYTCMDVFFHMADIFSVNITDQSGNYSQ 107
DB 59 RLXYQLVF--LLSAHTC-----IPENNAGAGCVCHL-----LMDDVVSAD-----NYTL 101
QY 108 EC-----GSFLAESIKPAPPPVTV--TFSGYINISMSDVEDPAFYMLKGLOLY 156
DB 102 DLWAGQQLMKWGSFKESEHVKPPAPGMLTVHTVNSDITLLTWSNPY--PPDNYLYNHLTY 159
QY 157 ELOYRNRGDMWNASPRKLSVDSRSVSLPLE-----PRKSSYELQVAPGMPG 207
DB 160 AVNIWSENDP-----APRIYVTVYLEBSLRIASTLKGSIYARARAW---A 205
QY 208 SSYQGTSEMSDPVIFOTOSHELKEGNNPHLLLVIVIFIPAFWSLKTHPMLRMKXI 267
DB 206 QCYNTTSEMSPESTKMH--NSYREPREQHLILGVSSCVILAVCLCVSITIKIKEM 262
QY 268 W-AVSPDEREFM-----PLYKC-----S 285
DB 263 WDQIPNPARSLVAIIIQDAQSQWMEKRSRGQEPAPKCPHKNGCLTKLLPCFLBNMKRDE 322
QY 286 GDFPKWVGAPFTGSLLEGWSP--EV-----BSTLEVYSCHPSPSPAKRLQLTQLOE-P 337
DB 323 DPHAAKEMFPQSG--KSAMCPVEISKTVLMBESISVVR-----VELFEAP 368
QY 338 AEIVESDGV--PKSFPMTAONSGGSAVSEERDRPYGLVSIIDTVTLDAEG----- 386
DB 369 VEEHEEVEEBKGSFCASSPSSRD--FGGREG--GIVARLESJLFLDLGEEENGFCQ 424
QY 387 -----PCTWPCSCED-----DGYPALDLDAG-----LEBPG----- 413
DB 425 QDMGESCLLPSPSGTSAHMPWDEFPS---AGKEAPPMWKEOPLHLEBPSPASPTQSPD 480
QY 414 -----LEBDPLDAGTVV--LSCGVASGSPGLGP---LGLSLDLRLKP----- 451
DB 481 NLCTETPLVIAQNPAYRSPSNLSOSPCCRELGPDPDLRLHLEVEPEMPCVPQJSEPT 540
QY 452 --PLADGEDW-----AGGLPMGGRSPG--GVSESEAG--SPLAGL----- 485
DB 541 TVQOPREPTWEOILRRNVLOHGAALAAVSAFPTSGYGEFVIAVQGGTQASAVVGLGPPGE 600
QY 486 -DMTDFSGFVSGDCSSPVECDFTS-----PDGSPSPSYLRQWVVIIP 527
DB 601 AGYKAF--SSLASAVSPKCGFASGEGYKPFODLIPGCGDPAF-----VP 649

OY 528 PLSPPG-----POAS 538
DB 650 VPLFTFGLDREPPRSPSS 668

RESULT 15

US-10-511-937-3001
Sequence 3001, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT FILING DATE: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3001
LENGTH: 825
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-3001

Query Match 6.5%; Score 193.5; DB 6; Length 825;
Best Local Similarity 21.8%; Pred. No. 2e-07;
Matches 161; Conservative 69; Mismatches 220; Indels 289; Gaps 42;

OY 17 GWCGRDLY-----CYTDVLYQVLCLEMMNLHPST-----L 47
DB 2 GMLCSGLLPVSCVLQVASSGNNKVLQEPCTVSDYMSISTC--EKKMNGPTNCSTEL 58
OY 48 TLTWDOYEELKDEATSCSLHRSANATHATYTCMDVHFHMADDIFSVNITDQSNYSQ 107
DB 59 RLXYQLV--LISEAHTC---IPENNGAGCVCHL-----LMDVVSAD-----NYTL 101
OY 108 EC-----GSFLAESIKPAPFNVTV--TSGQYNISMRSDYEDPAFYMLKGLQY 156
DB 102 DLMAGQQLLMKGSFSPSEHKVPRAAGNLTVHTNVSDDLTLTWSNRY--PPDNYLYNHLTY 159
OY 157 ELQYRNKDDPMAVSPRKLIVSDRSVSLPLE-----FRKDSYELQVAPAGPMFG 207
DB 160 AVNIMSENDP-----ADFRIVNYTVLEPSLRIAASTLKSISYRAVRAM---A 205
OY 208 SSYOGTSEMSDPIVYFOTQSEELKEGNPHLLLLLVIFIPAFWSLKTHTPLMRMKXI 267
DB 206 QCYVTTMSEMSPTKMH---NSYRPFQHLILGVSVCIVILAVCLCYVSIITIKKEW 262
OY 268 W-AVSPSPRPFM-----PLYKGC-----S 285
DB 263 WDOIENPARSLVALIIODAQSQWEKRSRGQEPKCPHMKCLTKLPCFLEHMKRDE 322
OY 286 GDFKRWVAPFTGSLLELGPWSP--EV-----PSTLEVYSCHPPRSAPAKRLQTLTELQ--P 337
DB 323 DPHKAAKEMPFQSG--KSAMCPVEISIKTVLWESISIVRC-----VELFEAP 368
OY 338 AELVESDGV--PKPSFMPTAONSGSAYSEERDRPYGLVSDITVTV--LDAEG----- 386
DB 369 VECSEEEVEEBEKSGFSCAPSSSRDD--FOEGRE---GIVARLTESTLFDLGEENGRCFQ 424

OY 387 -----PCTWPCSCBD-----DGYPALDLADG-----LEPSDG----- 413
DB 425 QDMGESCLPPSGSTSAHMPWDERPS-----AGPEAPRWGKEQPLHLEPSFPASTQSPD 480
OY 414 -----LEBDPLDAGTTV--LSCGVSAGSPGLGSP--LGLDLRLKP----- 451
DB 481 NLCTETPLVIAGNPAVRSFNSLSQSPCPRELGPDPILLARHLEBEVDEMPCPQLSEPT 540
OY 452 --PLADGEDW-----AGGLPWGKRSFG--GVSESEAG--SPLAGL----- 485
DB 541 TVQPPEPETWEQILRRNVLOHGAAPVSAFTSGYQEFVHAVBOGTOASAVVGLGPPGE 600
OY 486 -DMDFDPSGFVSGDSCSPVECDFTS-----PGDEGPPRSYLRQWVYIP 527
DB 601 AGYRAF--SSLASAVSBEKCGFASGSEBGRFPQDLIPCGPDDPAP-----VP 649
OY 528 PLSPPG-----POAS 538
DB 650 VPLFTFGLDREPPRSPSS 668

Search completed: September 7, 2006, 12:58:47
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